GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: January 19, 2005, 13:25:53 ; Search time 3903 Seconds
(without alignments)
9663.111 Million cell updates/sec

Title: US-09-913-772-1
Perfect score: 1035
Sequence: 1 atgaaagcaatttтcgtact.....taactcagccggcgggttaa 1035

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	461.6	44.6	671	7	CF558062	CF558062 1115033F0
	2	454.8	43.9	628	7	CF565551	CF565551 1115101B0
c	3	426	41.2	639	7	CF565552	CF565552 1115101B0
c	4	396	38.3	591	7	CF558063	CF558063 1115033F0
c	5	384.2	37.1	767	9	CL656958	CL656958 PRI0128a_
	6	274	26.5	422	7	CF561913	CF561913 1115069D0
	7	265.4	25.6	438	7	CF563205	CF563205 1115082A0
c	8	219	21.2	730	9	CL657503	CL657503 PRI0129d_
c	9	176	17.0	323	7	CF563206	CF563206 1115082A0
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c	11	134.2	13.0	655	8	AF075794	AF075794 AF075794
	12	61.4	5.9	601	7	CF915072	CF915072 B0973F11-
	13	61.4	5.9	601	7	CF915603	CF915603 B0982E05-
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	15	61.4	5.9	763	7	CK326686	CK326686 Hd_mx24_0
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c	18	54.8	5.3	748	8	BZ570213	BZ570213 msh2_1236
c	19	54.8	5.3	1030	8	BZ554003	BZ554003 pacs1-60_
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c	25	48.6	4.7	651	8	BZ566271	BZ566271 pacs2-164
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c	45	39.4	3.8	533	4	BJ192697	BJ192697 BJ192697

ALIGNMENTS

RESULT 1
CF558062
LOCUS CF558062 671 bp mRNA linear EST 23-SEP-2003
DEFINITION 1115033F05.x1 C. reinhardtii CC-1690 (mt+), Stress III (normalized), Lambda Zap II Chlamydomonas reinhardtii cDNA 3', mRNA sequence.
ACCESSION CF558062
VERSION CF558062.1 GI:34984145
KEYWORDS EST.
SOURCE Chlamydomonas reinhardtii
ORGANISM Chlamydomonas reinhardtii
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales; Chlamydomonadaceae; Chlamydomonas.
REFERENCE 1 (bases 1 to 671)
AUTHORS Grossman,A., Chang,C.-W., Davies,J., Harris,E., Hauser,C., Merchant,S., Quinn,J. and Shrager,J.
TITLE Analyses of the Chlamydomonas reinhardtii Genome: A Model, Unicellular System for Analyzing Gene Function and Regulation in Vascular Plants. Project: 1115
JOURNAL Unpublished (2003)
COMMENT Contact: Charles Hauser
DCMB Box 91000
Duke University
Durham, NC 27708-1000
Tel: 919 613 8159
Fax: 919 613 8177
Email: chauser@duke.edu
High quality sequence stop: 671.
FEATURES Location/Qualifiers
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/mol_type="mRNA"
/strain="CC-1690 wild type mt+ 21gr"
/db_xref="taxon:3055"
/clone_lib="C. reinhardtii CC-1690 (mt+), Stress III (normalized), Lambda Zap II"
/note="Vector: pBluescript II SK-; Site_1: EcoRI; Site_2: XhoI; Stress condition III library, constructed by Jeanette Quinn and Chiung-Wen Chang, combines cDNAs from CC-1690 cells grown to mid-log phase in copper-free TAP medium (see Quinn and Merchant(1998) Methods in Enzymology, 2997:263-279)in a shaking(250 rpm) illuminated (about 100 micromole/m2/sec) incubator at 22 C (see Quinn and Merchant(1998) Methods in Enzymology, 2997:263-279); CC-1690 cells grown to mid-log phase in low Fe (1 micromolar Fe) TAP medium (see La Fontaine S, Quinn JM, Nakamoto SS, Page MD, Gohre V, Moseley JL, Kropat J,

Merchant S.LaFontaine et al. (2002) Eukaryotic Cell, 1:736-757) in a shaking illuminated incubator (same conditions as above). CC-1690 cells were grown to mid-log phase in TAP medium in a shaking illuminated incubator to a density of 8x10e6 cells/ml. The flask was transferred to a shaking platform (200 rpm) at room temperature (23C) 12 micromole/m2/sec illumination and bubbled in a stoppered flask with 98% nitrogen, 2% CO2 gas mixture for 1 hour prior to harvesting for RNA isolation (as per Quinn JM, Barraco P, Eriksson M, Merchant S. Quinn et al. (2000) JBC 275:6080-6089); CC-1690 cells grown to mid-log phase (3x10e6 cells/ml) in TAP medium in a shaking (150 rpm) illuminated (70 mole photon/m2/sec) incubator at 27 C. Cells were diluted to 1x10e6 cells/ml, transferred to high light (11000 mol photon/m2/s) with shaking (150 rpm) and sampled at (0.5, 1,2,4,6, 12 hrs); CC-1690 cells grown to mid-log phase in HS medium in a shaking (150 rpm) illuminated (70 mole photon/m2/sec) incubator at 27 C. Cells were diluted to 1x10e6 cells/ml, transferred to high light (11000 mol photon/m2/s) with shaking (150 rpm) and sampled at (0.5, 1,2,4,6, 12 hrs). PolyA mRNA was purified from each sample, pooled and cDNA synthesized (see Shrager et al, Plant Physiol. 131, 401-408 for details). The cDNA was directionally cloned into lambda Zap II (Stratagene) in the EcoRI (5') and XhoRI (3') sites. pBluescript II SK- plasmids were excised from the lambda ZAP clones by superinfection with ExAssist (Stratagene) phage. The library was normalized using method 4 described in Bonaldo et al., (1996) Genome Research 6: 791-806."

ORIGIN

Query Match 44.6%; Score 461.6; DB 7; Length 671;
Best Local Similarity 83.3%; Pred. No. 5.7e-124;
Matches 543; Conservative 0; Mismatches 94; Indels 15; Gaps 1;

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Db        155 AAGCTCAGGGCGTTCAACTGACCGCTAAACTGGGTTACCCAATCACTGACGACCTGGACA 214

Qy        320 TCTACACCCGTCTGGGCGGCATGGTTTGGCGCGCTGACTCCAAAGGCAACTACGCTTCTA 379
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Qy        380 CCGGCGTTTCCCGTAGCGAACACGACACTGGCGTTTCCCCAGTATTTGCTGGCGGCGTAG 439
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Db        264 ----CGTTTATGGTAAAAACCACGACACCGGCGTTTCTCCGGTCTTCGCTGGCGGTGTTG 319

Qy        440 AGTGGGCTGTTACTCGTGACATCGCTACCCGTCTGGAATACCAGTGGGTTAACAACATCG 499
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Qy        500 GCGACGCGGGCACTGTGGGTACCCGTCCTGATAACGGCATGCTGAGCCTGGGCGTTTCCT 559
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Db        440 ACCGTTTCGGTCAGGGCGAAGCAGCTCCAGTAGTTGCTCCGGCTCCAGCTCCGGCACCGG 499

Qy        620 AAGTGGCTACCAAGCACTTCACCCTGAAGTCTGACGTTCTGTTCAACTTCAACAAAGCTA 679
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Db        500 AAGTACAGACCAAGCACTTCACTCTGAAGTCTGACGTTCTGTTCAACTTCAACAAAGCAA 559

Qy        680 CCCTGAAACCGGAAGGTCAGCAGGCTCTGGATCAGCTGTACACTCAGCTGAGCAACATGG 739
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Db        560 CCCTGAAACCGGAAGGTCAGGCTGCTCTGGATCAGCTGTACAGCCAGCTGAGCAACCTGG 619

Qy        740 ATCCGAAAGACGGTTCCGCTGTTGTTCTGGGCTACACCGACCGCATCGGTTC 791
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RESULT 2
CF565551
LOCUS CF565551 628 bp mRNA linear EST 23-SEP-2003
DEFINITION 1115101B09.x1 C. reinhardtii CC-1690 (mt+), Stress III (normalized), Lambda Zap II Chlamydomonas reinhardtii cDNA 3', mRNA sequence.
ACCESSION CF565551
VERSION CF565551.1 GI:34991634
KEYWORDS EST.
SOURCE Chlamydomonas reinhardtii
ORGANISM Chlamydomonas reinhardtii
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales; Chlamydomonadaceae; Chlamydomonas.
REFERENCE 1 (bases 1 to 628)
AUTHORS Grossman,A., Chang,C.-W., Davies,J., Harris,E., Hauser,C., Merchant,S., Quinn,J. and Shrager,J.
TITLE Analyses of the Chlamydomonas reinhardtii Genome: A Model, Unicellular System for Analyzing Gene Function and Regulation in Vascular Plants. Project: 1115
JOURNAL Unpublished (2003)
COMMENT Contact: Charles Hauser
DCMB Box 91000
Duke University
Durham, NC 27708-1000
Tel: 919 613 8159
Fax: 919 613 8177
Email: chauser@duke.edu
High quality sequence stop: 628.
FEATURES Location/Qualifiers
source 1. .628
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/mol_type="mRNA"
/strain="CC-1690 wild type mt+ 21gr"
/db_xref="taxon:3055"
/clone_lib="C. reinhardtii CC-1690 (mt+), Stress III (normalized), Lambda Zap II"
/note="Vector: pBluescript II SK-; Site_1: EcoRI; Site_2: XhoI; Stress condition III library, constructed by Jeanette Quinn and Chiung-Wen Chang, combines cDNAs from CC-1690 cells grown to mid-log phase in copper-free TAP medium (see Quinn and Merchant(1998) Methods in Enzymology, 2997:263-279)in a shaking(250 rpm) illuminated (about 100 micromole/m2/sec) incubator at 22 C (see Quinn and Merchant(1998) Methods in Enzymology, 2997:263-279); CC-1690 cells grown to mid-log phase in low Fe (1 micromolar Fe) TAP medium (see La Fontaine S, Quinn JM, Nakamoto SS, Page MD, Gohre V, Moseley JL, Kropat J, Merchant S.LaFontaine et al. (2002) Eukaryotic Cell, 1:736-757) in a shaking illuminated incubator (same conditions as above). CC-1690 cells were grown to mid-log phase in TAP medium in a shaking illuminated incubator to a density of 8x10e6 cells/ml. The flask was transferred to a shaking platform (200 rpm) at room temperature (23C) 12 micromole/m2/sec illumination and bubbled in a stoppered flask with 98% nitrogen, 2% CO2 gas mixture for 1 hour prior to harvesting for RNA isolation (as per Quinn JM, Barraco P, Eriksson M, Merchant S. Quinn et al. (2000) JBC 275:6080-6089); CC-1690 cells grown to mid-log phase (3x10e6 cells/ml) in TAP medium in a shaking (150 rpm) illuminated (70 mole photon/m2/sec) incubator at 27 C. Cells were diluted to 1x10e6 cells/ml, transferred to high light (11000 mol photon/m2/s) with shaking (150 rpm) and sampled at (0.5, 1,2,4,6, 12 hrs); CC-1690 cells grown to mid-log phase in HS medium in a shaking (150 rpm) illuminated (70 mole photon/m2/sec) incubator at 27 C. Cells were diluted to 1x10e6 cells/ml, transferred to high

light (11000 mol photon/m2/s) with shaking (150 rpm) and sampled at (0.5, 1,2,4,6, 12 hrs). PolyA mRNA was purified from each sample, pooled and cDNA synthesized (see Shrager et al, Plant Physiol. 131, 401-408 for details). The cDNA was directionally cloned into lambda Zap II (Stratagene) in the EcoRI (5') and XhoRI (3') sites. pBluescript II SK- plasmids were excised from the lambda ZAP clones by superinfection with ExAssist (Stratagene) phage. The library was normalized using method 4 described in Bonaldo et al., (1996) Genome Research 6: 791-806."

ORIGIN

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Qy        385 GTTTCCCGTAGCGAACACGACACTGGCGTTTCCCCAGTATTTGCTGGCGGCGTAGAGTGG 444
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Db        467 CAGACCAAGCACTTCACTCTGAAGTCTGACGTTCTGTTCAACTTCAACAAAGCAACCCTG 526

Qy        685 AAACCGGAAGGTCAGCAGGCTCTGGATCAGCTGTACACTCAGCTGAGCAACATGGATCCG 744
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RESULT 3
CF565552/c

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DEFINITION  1115101B09.y1 C. reinhardtii CC-1690 (mt+), Stress III
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            sequence.
ACCESSION   CF565552
VERSION     CF565552.1  GI:34991635
KEYWORDS    EST.
SOURCE      Chlamydomonas reinhardtii
  ORGANISM  Chlamydomonas reinhardtii
            Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
            Chlamydomonadaceae; Chlamydomonas.
REFERENCE   1  (bases 1 to 639)
  AUTHORS   Grossman,A., Chang,C.-W., Davies,J., Harris,E., Hauser,C.,
            Merchant,S., Quinn,J. and Shrager,J.
  TITLE     Analyses of the Chlamydomonas reinhardtii Genome: A Model,
            Unicellular System for Analyzing Gene Function and Regulation in
            Vascular Plants. Project: 1115
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Charles Hauser
            DCMB Box 91000
            Duke University
            Durham, NC 27708-1000
            Tel: 919 613 8159
            Fax: 919 613 8177
            Email: chauser@duke.edu
            High quality sequence stop: 639.
FEATURES             Location/Qualifiers
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                     /strain="CC-1690 wild type mt+ 21gr"
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                     /clone_lib="C. reinhardtii CC-1690 (mt+), Stress III
                     (normalized), Lambda Zap II"
                     /note="Vector: pBluescript II SK-; Site_1: EcoRI; Site_2:
                     XhoI; Stress condition III library, constructed by
                     Jeanette Quinn and Chiung-Wen Chang, combines cDNAs from
                     CC-1690 cells grown to mid-log phase in copper-free TAP
                     medium (see Quinn and Merchant(1998) Methods in
                     Enzymology, 2997:263-279)in a shaking(250 rpm) illuminated
                     (about 100 micromole/m2/sec) incubator at 22 C (see Quinn
                     and Merchant(1998) Methods in Enzymology, 2997:263-279);
                     CC-1690 cells grown to mid-log phase in low Fe (1
                     micromolar Fe) TAP medium (see La Fontaine S, Quinn JM,
                     Nakamoto SS, Page MD, Gohre V, Moseley JL, Kropat J,
                     Merchant S.LaFontaine et al. (2002) Eukaryotic Cell,
                     1:736-757) in a shaking illuminated incubator (same
                     conditions as above). CC-1690 cells were grown to mid-log
                     phase in TAP medium in a shaking illuminated incubator to
                     a density of 8x10e6 cells/ml. The flask was transferred to
                     a shaking platform (200 rpm) at room temperature (23C) 12
                     micromole/m2/sec illumination and bubbled in a stoppered
                     flask with 98% nitrogen, 2% CO2 gas mixture for 1 hour
                     prior to harvesting for RNA isolation (as per Quinn JM,
                     Barraco P, Eriksson M, Merchant S. Quinn et al. (2000) JBC
                     275:6080-6089); CC-1690 cells grown to mid-log phase
                     (3x10e6 cells/ml) in TAP medium in a shaking (150 rpm)
                     illuminated (70 mole photon/m2/sec) incubator at 27 C.
                     Cells were diluted to 1x10e6 cells/ml, transferred to high
                     light (11000 mol photon/m2/s) with shaking (150 rpm) and
                     sampled at (0.5, 1,2,4,6, 12 hrs); CC-1690 cells grown to
                     mid-log phase in HS medium in a shaking (150 rpm)
                     illuminated (70 mole photon/m2/sec) incubator at 27 C.
                     Cells were diluted to 1x10e6 cells/ml, transferred to high
                     light (11000 mol photon/m2/s) with shaking (150 rpm) and
                     sampled at (0.5, 1,2,4,6, 12 hrs). PolyA mRNA was purified
                     from each sample, pooled and cDNA synthesized (see Shrager
                     et al, Plant Physiol. 131, 401-408 for details). The cDNA
                     was directionally cloned into lambda Zap II (Stratagene)
                     in the EcoRI (5') and XhoRI (3') sites. pBluescript II SK-
                     plasmids were excised from the lambda ZAP clones by
                     superinfection with ExAssist (Stratagene) phage. The
                     library was normalized using method 4 described in Bonaldo
                     et al., (1996) Genome Research 6: 791-806."
ORIGIN
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  Query Match            41.2%;  Score 426;  DB 7;  Length 639;
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  Matches  471;  Conservative    0;  Mismatches   75;  Indels    0;  Gaps    0;

Qy        490 AACAACATCGGCGACGCGGGCACTGTGGGTACCCGTCCTGATAACGGCATGCTGAGCCTG 549
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Qy        550 GGCGTTTCCTACCGCTTCGGTCAGGAAGATGCTGCACCGGTTGTTGCTCCGGCTCCGGCT 609
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Db        578 GGTGTTTCCTACCGTTTCGGTCAGGGCGAAGCAGCTCCAGTAGTTGCTCCGGCTCCAGCT 519

Qy        610 CCGGCTCCGGAAGTGGCTACCAAGCACTTCACCCTGAAGTCTGACGTTCTGTTCAACTTC 669
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Db        518 CCGGCACCGGAAGTACAGACCAAGCACTTCACTCTGAAGTCTGACGTTCTGTTCAACTTC 459

Qy        670 AACAAAGCTACCCTGAAACCGGAAGGTCAGCAGGCTCTGGATCAGCTGTACACTCAGCTG 729
              |||||||| |||||||||||||||||||   |||||||||||||||||  ||||||
Db        458 AACAAAGCAACCCTGAAACCGGAAGGTCAGGCTGCTCTGGATCAGCTGTACAGCCAGCTG 399

Qy        730 AGCAACATGGATCCGAAAGACGGTTCCGCTGTTGTTCTGGGCTACACCGACCGCATCGGT 789
              ||||||  |||||||||||||||||||||   |||||||||||  |||||||||||||||||
Db        398 AGCAACCTGGATCCGAAAGACGGTTCCGTAGTTGTTCTGGGTTACACCGACCGCATCGGT 339

Qy        790 TCCGAAGCTTACAACCAGCAGCTGTCTGAGAAACGTGCTCAGTCCGTTGTTGACTACCTG 849
              || || ||||||||||||   ||||| |||   |||||||||| |||||||| ||||||
Db        338 TCTGACGCTTACAACCAGGGTCTGTCCGAGCGCCGTGCTCAGTCTGTTGTTGATTACCTG 279

Qy        850 GTTGCTAAAGGCATCCCGGCTGGCAAAATCTCCGCTCGCGGCATGGGTGAATCCAACCCG 909
              |  | ||||| |||||||| | ||| |||||||| || || ||||| ||||| ||||||
Db        278 ATCTCCAAAGGTATCCCGGCAGACAAGATCTCCGCACGTGGTATGGGCGAATCTAACCCG 219

Qy        910 GTTACTGGCAACACCTGTGACAACGTGAAAGCTCGCGCTGCCCTGATCGATTGCCTGGCT 969
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Db        218 GTTACTGGCAACACCTGTGACAACGTGAAACAGCGTGCTGCACTGATCGACTGCCTGGCT 159

Qy        970 CCGGATCGTCGTGTAGAGATCGAAGTTAAAGGCTACAAAGAAGTTGTAACTCAGCCGGCG 1029
              |||||||||| |||||||||||||||||   |||||| ||||||||||||||| |
Db        158 CCGGATCGTCGCGTAGAGATCGAAGTTAAAGGTATCAAAGACGTTGTAACTCAGCCGCAG 99

Qy       1030 GGTTAA 1035
              | ||||
Db         98 GCTTAA 93
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RESULT 4
CF558063/c
LOCUS CF558063 591 bp mRNA linear EST 23-SEP-2003
DEFINITION 1115033F05.y1 C. reinhardtii CC-1690 (mt+), Stress III (normalized), Lambda Zap II Chlamydomonas reinhardtii cDNA 5', mRNA sequence.
ACCESSION CF558063
VERSION CF558063.1 GI:34984146
KEYWORDS EST.
SOURCE Chlamydomonas reinhardtii
ORGANISM Chlamydomonas reinhardtii
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales; Chlamydomonadaceae; Chlamydomonas.
REFERENCE 1 (bases 1 to 591)
AUTHORS Grossman,A., Chang,C.-W., Davies,J., Harris,E., Hauser,C., Merchant,S., Quinn,J. and Shrager,J.
TITLE Analyses of the Chlamydomonas reinhardtii Genome: A Model, Unicellular System for Analyzing Gene Function and Regulation in Vascular Plants. Project: 1115
JOURNAL Unpublished (2003)
COMMENT Contact: Charles Hauser
DCMB Box 91000
Duke University
Durham, NC 27708-1000
Tel: 919 613 8159
Fax: 919 613 8177
Email: chauser@duke.edu
High quality sequence stop: 591.
FEATURES Location/Qualifiers
source 1. .591
/organism="Chlamydomonas reinhardtii"
/mol_type="mRNA"
/strain="CC-1690 wild type mt+ 21gr"
/db_xref="taxon:3055"
/clone_lib="C. reinhardtii CC-1690 (mt+), Stress III (normalized), Lambda Zap II"
/note="Vector: pBluescript II SK-; Site_1: EcoRI; Site_2: XhoI; Stress condition III library, constructed by Jeanette Quinn and Chiung-Wen Chang, combines cDNAs from CC-1690 cells grown to mid-log phase in copper-free TAP medium (see Quinn and Merchant(1998) Methods in Enzymology, 2997:263-279)in a shaking(250 rpm) illuminated (about 100 micromole/m2/sec) incubator at 22 C (see Quinn and Merchant(1998) Methods in Enzymology, 2997:263-279); CC-1690 cells grown to mid-log phase in low Fe (1 micromolar Fe) TAP medium (see La Fontaine S, Quinn JM, Nakamoto SS, Page MD, Gohre V, Moseley JL, Kropat J, Merchant S.LaFontaine et al. (2002) Eukaryotic Cell, 1:736-757) in a shaking illuminated incubator (same conditions as above). CC-1690 cells were grown to mid-log phase in TAP medium in a shaking illuminated incubator to a density of 8x10e6 cells/ml. The flask was transferred to a shaking platform (200 rpm) at room temperature (23C) 12 micromole/m2/sec illumination and bubbled in a stoppered flask with 98% nitrogen, 2% CO2 gas mixture for 1 hour prior to harvesting for RNA isolation (as per Quinn JM, Barraco P, Eriksson M, Merchant S. Quinn et al. (2000) JBC 275:6080-6089); CC-1690 cells grown to mid-log phase (3x10e6 cells/ml) in TAP medium in a shaking (150 rpm) illuminated (70 mole photon/m2/sec) incubator at 27 C. Cells were diluted to 1x10e6 cells/ml, transferred to high light (11000 mol photon/m2/s) with shaking (150 rpm) and sampled at (0.5, 1,2,4,6, 12 hrs); CC-1690 cells grown to mid-log phase in HS medium in a shaking (150 rpm) illuminated (70 mole photon/m2/sec) incubator at 27 C. Cells were diluted to 1x10e6 cells/ml, transferred to high light (11000 mol photon/m2/s) with shaking (150 rpm) and sampled at (0.5, 1,2,4,6, 12 hrs). PolyA mRNA was purified from each sample, pooled and cDNA synthesized (see Shrager et al, Plant Physiol. 131, 401-408 for details). The cDNA was directionally cloned into lambda Zap II (Stratagene) in the EcoRI (5') and XhoRI (3') sites. pBluescript II SK- plasmids were excised from the lambda ZAP clones by superinfection with ExAssist (Stratagene) phage. The library was normalized using method 4 described in Bonaldo et al., (1996) Genome Research 6: 791-806."
ORIGIN

Query Match 38.3%; Score 396; DB 7; Length 591;
Best Local Similarity 87.0%; Pred. No. 9.8e-105;
Matches 435; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

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Qy        536 GCATGCTGAGCCTGGGCGTTTCCTACCGCTTCGGTCAGGAAGATGCTGCACCGGTTGTTG 595
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Db        591 GCATGCTGATCCTGGGTGTTTCTTACCGTTTCGGTCAGGGCGAAGCAGCCCCAGTAGTTG 532

Qy        596 CTCCGGCTCCGGCTCCGGCTCCGGAAGTGGCTACCAAGCACTTCACCCTGAAGTCTGACG 655
              |||||||||| |||||||| ||||||||    |||||||||||||| ||||||||||||
Db        531 CTCCGGCTCCAGCTCCGGCACCGGAAGTACAGACCAAGCACTTCACTCTGAAGTCTGACG 472

Qy        656 TTCTGTTCAACTTCAACAAAGCTACCCTGAAACCGGAAGGTCAGCAGGCTCTGGATCAGC 715
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Db        471 TTCTGTTCAACTTCAACAAAGCAACCCTGAAACCGGAAGGTCAGGCTGCTCTGGATCAGC 412

Qy        716 TGTACACTCAGCTGAGCAACATGGATCCGAAAGACGGTTCCGCTGTTGTTCTGGGCTACA 775
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Db        411 TGTACAGCCAGCTGAGCAACCTGGATCCGAAAGACGGTTCCGTAGTTGTTCTGGGTTACA 352

Qy        776 CCGACCGCATCGGTTCCGAAGCTTACAACCAGCAGCTGTCTGAGAAACGTGCTCAGTCCG 835
              |||||||||||||||| || ||||||||||||   ||||| |||   |||||||||| |
Db        351 CCGACCGCATCGGTTCTGACGCTTACAACCAGGGTCTGTCCGAGCGCCGTGCTCAGTCTG 292

Qy        836 TTGTTGACTACCTGGTTGCTAAAGGCATCCCGGCTGGCAAAATCTCCGCTCGCGGCATGG 895
              |||||||  |||||| |  | |||||  |||||||| | |||  |||||||| || || ||||
Db        291 TTGTTGATTACCTGATCTCCAAAGGTATCCCGGCAGACAAGATCTCCGCACGTGGTATGG 232

Qy        896 GTGAATCCAACCCGGTTACTGGCAACACCTGTGACAACGTGAAAGCTCGCGCTGCCCTGA 955
              | ||||||||||||||||||||||||||||||||||||||||||||   || ||||| ||||
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Db        231 GCGAATCCAACCCGGTTACTGGCAACACCTGTGACAACGTGAAACAGCGTGCTGCACTGA 172

Qy        956 TCGATTGCCTGGCTCCGGATCGTCGTGTAGAGATCGAAGTTAAAGGCTACAAAGAAGTTG 1015
              |||| |||||||||||||||||||| ||||||||||||||||||||   |||||| ||||
Db        171 TCGACTGCCTGGCTCCGGATCGTCGCGTAGAGATCGAAGTTAAAGGTATCAAAGACGTTG 112

Qy       1016 TAACTCAGCCGGCGGGTTAA 1035
              ||||||||||| || ||||
Db        111 TAACTCAGCCGCAGGCTTAA 92


RESULT 5
CL656958/c
LOCUS       CL656958                767 bp    DNA     linear   GSS 09-JUL-2004
DEFINITION  PRI0128a_C05 - PRI0128a.B21 (767) Mixed stage fosmid library of P.
            pacificus var. California Pristionchus pacificus genomic, genomic
            survey sequence.
ACCESSION   CL656958
VERSION     CL656958.1  GI:50137970
KEYWORDS    GSS.
SOURCE      Pristionchus pacificus
  ORGANISM  Pristionchus pacificus
            Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
            Neodiplogasteridae; Pristionchus.
REFERENCE   1  (bases 1 to 767)
  AUTHORS   Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
  TITLE     AppaDB: an AcedB database for the nematode satellite organism
            Pristionchus pacificus
  JOURNAL   Nucleic Acids Res. 32 (1), D421-D422 (2004)
COMMENT     Contact: Sommer RJ
            Evolutionary Biology
            Max-Planck-Institute for Developmental Biology
            Spemannstr. 37-39, Tuebingen D-72076, Germany
            Tel: 00497071601371
            Fax: 00497071601498
            Email: ralf.sommer@tuebingen.mpg.de
            This library was generated at Caltech, Pasadena, USA and end
            sequenced at Vancouver, Canada.
            Seq primer: T7
            Class: fosmid ends.
FEATURES             Location/Qualifiers
     source          1. .767
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                     /mol_type="genomic DNA"
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                     var. California"
                     /note="Vector: pEpifos-5 Fosmid vector"
ORIGIN

  Query Match             37.1%;  Score 384.2;  DB 9;  Length 767;
  Best Local Similarity   87.0%;  Pred. No. 3.1e-101;
  Matches  422;  Conservative    0;  Mismatches   63;  Indels    0;  Gaps    0;

Qy        551 GCGTTTCCTACCGCTTCGGTCAGGAAGATGCTGCACCGGTTGTTGCTCCGGCTCCGGCTC 610
              | |||||||||||| ||||||||||  || || || || || ||||||||||||| ||||
Db        767 GTGTTTCCTACCGTTTCGGTCAGGGCGAAGCAGCTCCAGTAGTTGCTCCGGCTCCAGCTC 708

Qy        611 CGGCTCCGGAAGTGGCTACCAAGCACTTCACCCTGAAGTCTGACGTTCTGTTCAACTTCA 670
              |||| ||||||||    |||||||||||||| |||||||||||||||||||||||||||||
Db        707 CGGCACCGGAAGTACAGACCAAGCACTTCACTCTGAAGTCTGACGTTCTGTTCAACTTCA 648

Qy        671 ACAAAGCTACCCTGAAACCGGAAGGTCAGCAGGCTCTGGATCAGCTGTACACTCAGCTGA 730
              ||||||| |||||||||||||||||||   |||||||||||||||||||  |||||||
Db        647 ACAAAGCAACCCTGAAACCGGAAGGTCAGGCTGCTCTGGATCAGCTGTACAGCCAGCTGA 588

Qy        731 GCAACATGGATCCGAAAGACGGTTCCGCTGTTGTTCTGGGCTACACCGACCGCATCGGTT 790
              ||||| |||||||||||||||||||  |||||||||| |||||||||||||||||||||
Db        587 GCAACCTGGATCCGAAAGACGGTTCCGTAGTTGTTCTGGGTTACACCGACCGCATCGGTT 528

Qy        791 CCGAAGCTTACAACCAGCAGCTGTCTGAGAAACGTGCTCAGTCCGTTGTTGACTACCTGG 850
              | || ||||||||||||   ||||| |||   |||||||||| |||||||| ||||||

Db        527 CTGACGCTTACAACCAGGGTCTGTCCGAGCGCCGTGCTCAGTCTGTTGTTGATTACCTGA 468

Qy        851 TTGCTAAAGGCATCCCGGCTGGCAAAATCTCCGCTCGCGGCATGGGTGAATCCAACCCGG 910
              | | ||||| |||||||| | ||| |||||||| || || ||||| ||||||||||||||
Db        467 TCTCCAAAGGTATCCCGGCAGACAAGATCTCCGCACGTGGTATGGGCGAATCCAACCCGG 408

Qy        911 TTACTGGCAACACCTGTGACAACGTGAAAGCTCGCGCTGCCCTGATCGATTGCCTGGCTC 970
              |||||||||||||||||||||||||||||||   || ||||| |||||||| ||||||||||
Db        407 TTACTGGCAACACCTGTGACAACGTGAAACAGCGTGCTGCACTGATCGACTGCCTGGCTC 348

Qy        971 CGGATCGTCGTGTAGAGATCGAAGTTAAAGGCTACAAAGAAGTTGTAACTCAGCCGGCGG 1030
              |||||||||| ||||||||||||||||||||   |||||| ||||||||||||||||  ||
Db        347 CGGATCGTCGCGTAGAGATCGAAGTTAAAGGTATCAAAGACGTTGTAACTCAGCCGCAGG 288

Qy       1031 GTTAA 1035
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Db        287 CTTAA 283


RESULT 6
CF561913
LOCUS       CF561913                422 bp    mRNA    linear   EST 23-SEP-2003
DEFINITION  1115069D01.x1 C. reinhardtii CC-1690 (mt+), Stress III
            (normalized), Lambda Zap II Chlamydomonas reinhardtii cDNA 3', mRNA
            sequence.
ACCESSION   CF561913
VERSION     CF561913.1  GI:34987996
KEYWORDS    EST.
SOURCE      Chlamydomonas reinhardtii
  ORGANISM  Chlamydomonas reinhardtii
            Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
            Chlamydomonadaceae; Chlamydomonas.
REFERENCE   1  (bases 1 to 422)
  AUTHORS   Grossman,A., Chang,C.-W., Davies,J., Harris,E., Hauser,C.,
            Merchant,S., Quinn,J. and Shrager,J.
  TITLE     Analyses of the Chlamydomonas reinhardtii Genome: A Model,
            Unicellular System for Analyzing Gene Function and Regulation in
            Vascular Plants. Project: 1115
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Charles Hauser
            DCMB Box 91000
            Duke University
            Durham, NC 27708-1000
            Tel: 919 613 8159
            Fax: 919 613 8177
            Email: chauser@duke.edu
            High quality sequence stop: 422.
FEATURES             Location/Qualifiers
     source          1. .422
                     /organism="Chlamydomonas reinhardtii"
                     /mol_type="mRNA"
                     /strain="CC-1690 wild type mt+ 21gr"
                     /db_xref="taxon:3055"
                     /clone_lib="C. reinhardtii CC-1690 (mt+), Stress III
                     (normalized), Lambda Zap II"
                     /note="Vector: pBluescript II SK-; Site_1: EcoRI; Site_2:
                     XhoI; Stress condition III library, constructed by
                     Jeanette Quinn and Chiung-Wen Chang, combines cDNAs from
                     CC-1690 cells grown to mid-log phase in copper-free TAP
                     medium (see Quinn and Merchant(1998) Methods in
                     Enzymology, 2997:263-279)in a shaking(250 rpm) illuminated
                     (about 100 micromole/m2/sec) incubator at 22 C (see Quinn
                     and Merchant(1998) Methods in Enzymology, 2997:263-279);
                     CC-1690 cells grown to mid-log phase in low Fe (1
                     micromolar Fe) TAP medium (see La Fontaine S, Quinn JM,
                     Nakamoto SS, Page MD, Gohre V, Moseley JL, Kropat J,
                     Merchant S.LaFontaine et al. (2002) Eukaryotic Cell,
                     1:736-757) in a shaking illuminated incubator (same
                     conditions as above). CC-1690 cells were grown to mid-log
                     phase in TAP medium in a shaking illuminated incubator to
                     a density of 8x10e6 cells/ml. The flask was transferred to
                     a shaking platform (200 rpm) at room temperature (23C) 12
                     micromole/m2/sec illumination and bubbled in a stoppered
```

flask with 98% nitrogen, 2% CO2 gas mixture for 1 hour prior to harvesting for RNA isolation (as per Quinn JM, Barraco P, Eriksson M, Merchant S. Quinn et al. (2000) JBC 275:6080-6089); CC-1690 cells grown to mid-log phase (3x10e6 cells/ml) in TAP medium in a shaking (150 rpm) illuminated (70 mole photon/m2/sec) incubator at 27 C. Cells were diluted to 1x10e6 cells/ml, transferred to high light (11000 mol photon/m2/s) with shaking (150 rpm) and sampled at (0.5, 1,2,4,6, 12 hrs); CC-1690 cells grown to mid-log phase in HS medium in a shaking (150 rpm) illuminated (70 mole photon/m2/sec) incubator at 27 C. Cells were diluted to 1x10e6 cells/ml, transferred to high light (11000 mol photon/m2/s) with shaking (150 rpm) and sampled at (0.5, 1,2,4,6, 12 hrs). PolyA mRNA was purified from each sample, pooled and cDNA synthesized (see Shrager et al, Plant Physiol. 131, 401-408 for details). The cDNA was directionally cloned into lambda Zap II (Stratagene) in the EcoRI (5') and XhoRI (3') sites. pBluescript II SK- plasmids were excised from the lambda ZAP clones by superinfection with ExAssist (Stratagene) phage. The library was normalized using method 4 described in Bonaldo et al., (1996) Genome Research 6: 791-806."

ORIGIN

Query Match 26.5%; Score 274; DB 7; Length 422;
Best Local Similarity 79.3%; Pred. No. 5.8e-69;
Matches 344; Conservative 0; Mismatches 75; Indels 15; Gaps 1;

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Qy        128 CGACCCGTAACGATCAGCTTGGTGCTGGTGCGTTCGGTGGTTACCAGGTTAACCCGTACC 187
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Db          4 CGACCCATGAAAACCAACTGGGCGCTGGTGCTTTTGGTGGTTACCAGGTTAACCCGTATG 63

Qy        188 TCGGTTTCGAAATGGGTTATGACTGGCTGGGCCGTATGGCATATAAAGGCAGCGTTGACA 247
              | || || |||||||||||| |||||| | || |||||| | || |||||||||||||| |
Db         64 TTGGCTTTGAAATGGGTTACGACTGGTTAGGTCGTATGCCGTACAAAGGCAGCGTTGAAA 123

Qy        248 ACGGTGCTTTCAAAGCTCAGGGCGTTCAGCTGACCGCTAAACTGGGTTACCCGATCACTG 307
              ||||||| | |||||||||||||||||| |||||||||||||||||||||||| |||||||
Db        124 ACGGTGCATACAAAGCTCAGGGCGTTCAACTGACCGCTAAACTGGGTTACCCAATCACTG 183

Qy        308 ACGATCTGGACATCTACACCCGTCTGGGCGGCATGGTTTGGCGCGCTGACTCCAAAGGCA 367
              |||| |||||||||||||| |||||||| |||||||| ||||| || ||| | |||  ||
Db        184 ACGACCTGGACATCTACACTCGTCTGGGTGGCATGGTATGGCGTGCAGACACTAAATCCA 243

Qy        368 ACTACGCTTCTACCGGCGTTTCCCGTAGCGAACACGACACTGGCGTTTCCCCAGTATTTG 427
              |                |||||   |||   | |||||||| |||||||| || || || |
Db        244 A---------------CGTTTATGGTAAAAACCACGACACCGGCGTTTCTCCGGTCTTCG 288

Qy        428 CTGGCGGCGTAGAGTGGGCTGTTACTCGTGACATCGCTACCCGTCTGGAATACCAGTGGG 487
              ||||||| || ||||  ||  | |||| ||| ||||||||||||||||||||||||||
Db        289 CTGGCGGTGTTGAGTACGCGATCACTCCTGAAATCGCTACCCGTCTGGAATACCAGTGGA 348

Qy        488 TTAACAACATCGGCGACGCGGGCACTGTGGGTACCCGTCCTGATAACGGCATGCTGAGCC 547
              |||||||||||| |||||   |||  | || || | ||| || ||||||||||||| |
Db        349 CCAACAACATCGGTGACGCACACACCATCGGCACTCTTCCGGACAACGGCATGCTGAGTC 408

Qy        548 TGGGCGTTTCCTAC 561
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Db        409 TGGGTGTTTCCTAC 422
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RESULT 7
CF563205
LOCUS CF563205 438 bp mRNA linear EST 23-SEP-2003
DEFINITION 1115082A08.x1 C. reinhardtii CC-1690 (mt+), Stress III (normalized), Lambda Zap II Chlamydomonas reinhardtii cDNA 3', mRNA sequence.
ACCESSION CF563205
VERSION CF563205.1 GI:34989288
KEYWORDS EST.
SOURCE Chlamydomonas reinhardtii
ORGANISM Chlamydomonas reinhardtii
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales; Chlamydomonadaceae; Chlamydomonas.
REFERENCE 1 (bases 1 to 438)
AUTHORS Grossman,A., Chang,C.-W., Davies,J., Harris,E., Hauser,C., Merchant,S., Quinn,J. and Shrager,J.
TITLE Analyses of the Chlamydomonas reinhardtii Genome: A Model, Unicellular System for Analyzing Gene Function and Regulation in Vascular Plants. Project: 1115
JOURNAL Unpublished (2003)
COMMENT Contact: Charles Hauser
DCMB Box 91000
Duke University
Durham, NC 27708-1000
Tel: 919 613 8159
Fax: 919 613 8177
Email: chauser@duke.edu
High quality sequence stop: 438.
FEATURES Location/Qualifiers
source 1. .438
/organism="Chlamydomonas reinhardtii"
/mol_type="mRNA"
/strain="CC-1690 wild type mt+ 21gr"
/db_xref="taxon:3055"
/clone_lib="C. reinhardtii CC-1690 (mt+), Stress III (normalized), Lambda Zap II"
/note="Vector: pBluescript II SK-; Site_1: EcoRI; Site_2: XhoI; Stress condition III library, constructed by Jeanette Quinn and Chiung-Wen Chang, combines cDNAs from CC-1690 cells grown to mid-log phase in copper-free TAP medium (see Quinn and Merchant(1998) Methods in Enzymology, 2997:263-279)in a shaking(250 rpm) illuminated (about 100 micromole/m2/sec) incubator at 22 C (see Quinn and Merchant(1998) Methods in Enzymology, 2997:263-279); CC-1690 cells grown to mid-log phase in low Fe (1 micromolar Fe) TAP medium (see La Fontaine S, Quinn JM, Nakamoto SS, Page MD, Gohre V, Moseley JL, Kropat J, Merchant S.LaFontaine et al. (2002) Eukaryotic Cell, 1:736-757) in a shaking illuminated incubator (same conditions as above). CC-1690 cells were grown to mid-log phase in TAP medium in a shaking illuminated incubator to a density of 8x10e6 cells/ml. The flask was transferred to a shaking platform (200 rpm) at room temperature (23C) 12 micromole/m2/sec illumination and bubbled in a stoppered flask with 98% nitrogen, 2% CO2 gas mixture for 1 hour prior to harvesting for RNA isolation (as per Quinn JM, Barraco P, Eriksson M, Merchant S. Quinn et al. (2000) JBC 275:6080-6089); CC-1690 cells grown to mid-log phase (3x10e6 cells/ml) in TAP medium in a shaking (150 rpm) illuminated (70 mole photon/m2/sec) incubator at 27 C. Cells were diluted to 1x10e6 cells/ml, transferred to high light (11000 mol photon/m2/s) with shaking (150 rpm) and sampled at (0.5, 1,2,4,6, 12 hrs); CC-1690 cells grown to mid-log phase in HS medium in a shaking (150 rpm) illuminated (70 mole photon/m2/sec) incubator at 27 C. Cells were diluted to 1x10e6 cells/ml, transferred to high light (11000 mol photon/m2/s) with shaking (150 rpm) and sampled at (0.5, 1,2,4,6, 12 hrs). PolyA mRNA was purified from each sample, pooled and cDNA synthesized (see Shrager et al, Plant Physiol. 131, 401-408 for details). The cDNA was directionally cloned into lambda Zap II (Stratagene) in the EcoRI (5') and XhoRI (3') sites. pBluescript II SK- plasmids were excised from the lambda ZAP clones by superinfection with ExAssist (Stratagene) phage. The library was normalized using method 4 described in Bonaldo et al., (1996) Genome Research 6: 791-806."

ORIGIN

Query Match 25.6%; Score 265.4; DB 7; Length 438;
Best Local Similarity 78.7%; Pred. No. 1.9e-66;
Matches 336; Conservative 0; Mismatches 76; Indels 15; Gaps 1;

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Qy        130 ACCCGTAACGATCAGCTTGGTGCTGGTGCGTTCGGTGGTTACCAGGTTAACCCGTACCTC 189
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Db         27 AACCATGAAAACCAACTGGGCGCTGGTGCTTTTGGTGGTTACCAGGTTAACCCGTATGTT 86
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Qy        190 GGTTTCGAAATGGGTTATGACTGGCTGGGCCGTATGGCATATAAAGGCAGCGTTGACAAC 249
              || || ||||||||||| |||||| | || |||||| | || ||||||||||||||| |||
Db         87 GGCTTTGAAATGGGTTACGACTGGTTAGGTCGTATGCCGTACAAAGGCAGCGTTGAAAAC 146

Qy        250 GGTGCTTTCAAAGCTCAGGGCGTTCAGCTGACCGCTAAACTGGGTTACCCGATCACTGAC 309
              ||||| | |||||||||||||||||| ||||||||||||||||||||||||| ||||||||
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Qy        310 GATCTGGACATCTACACCCGTCTGGGCGGCATGGTTTGGCGCGCTGACTCCAAAGGCAAC 369
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Qy        370 TACGCTTCTACCGGCGTTTCCCGTAGCGAACACGACACTGGCGTTTCCCCAGTATTTGCT 429
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Db        266 --------------CGTTTATGGTAAAAACCACGACACCGGCGTTTCTCCGGTCTTCGCT 311

Qy        430 GGCGGCGTAGAGTGGGCTGTTACTCGTGACATCGCTACCCGTCTGGAATACCAGTGGGTT 489
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Qy        490 AACAACATCGGCGACGCGGGCACTGTGGGTACCCGTCCTGATAACGGCATGCTGAGCCTG 549
              |||||||||| |||||   |||  | || || ||||| || ||||||||||||||||||
Db        372 AACAACATCGGTGACGCACACACCATCGGCACTCGTCCGGACAACGGCATGCTGAGCCTG 431

Qy        550 GGCGTTT 556
              || ||||
Db        432 GGTGTTT 438
```

RESULT 8
CL657503/c
LOCUS CL657503 730 bp DNA linear GSS 09-JUL-2004
DEFINITION PRI0129d_A09 - PRI0129d.B21 (730) Mixed stage fosmid library of P. pacificus var. California Pristionchus pacificus genomic, genomic survey sequence.
ACCESSION CL657503
VERSION CL657503.1 GI:50139169
KEYWORDS GSS.
SOURCE Pristionchus pacificus
ORGANISM Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida; Neodiplogasteridae; Pristionchus.
REFERENCE 1 (bases 1 to 730)
AUTHORS Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
TITLE AppaDB: an AcedB database for the nematode satellite organism Pristionchus pacificus
JOURNAL Nucleic Acids Res. 32 (1), D421-D422 (2004)
COMMENT Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end sequenced at Vancouver, Canada.
Seq primer: T7
Class: fosmid ends.
FEATURES Location/Qualifiers
source 1. .730
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/clone_lib="Mixed stage fosmid library of P. pacificus var. California"
/note="Vector: pEpifos-5 Fosmid vector"
ORIGIN

Query Match 21.2%; Score 219; DB 9; Length 730;
Best Local Similarity 85.9%; Pred. No. 9.4e-53;
Matches 243; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

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Qy        753 TTCCGCTGTTGTTCTGGGCTACACCGACCGCATCGGTTCCGAAGCTTACAACCAGCAGCT 812
              |||||  |||||||||| |||||||||||||||||||| || ||||||||||||   ||
Db        730 TTCCGTAGTTGTTCTGGGTTACACCGACCGCATCGGTTCTGACGCTTACAACCAGGGTCT 671

Qy        813 GTCTGAGAAACGTGCTCAGTCCGTTGTTGACTACCTGGTTGCTAAAGGCATCCCGGCTGG 872
              ||| |||   |||||||||| |||||||| |||||  |   | ||||| ||||||||  |
Db        670 GTCCGAGCGCCGTGCTCAGTCTGTTGTTGATTACCTGATCTCCAAAGGTATCCCGGCAGA 611

Qy        873 CAAAATCTCCGCTCGCGGCATGGGTGAATCCAACCCGGTTACTGGCAACACCTGTGACAA 932
              ||| ||||||||  || || ||||| ||||||||||||||||||||||||||||||||||
Db        610 CAAGATCTCCGCACGTGGTATGGGCGAATCCAACCCGGTTACTGGCAACACCTGTGACAA 551

Qy        933 CGTGAAAGCTCGCGCTGCCCTGATCGATTGCCTGGCTCCGGATCGTCGTGTAGAGATCGA 992
              |||||||   || ||||| |||||||| ||||||||||||||||||| ||||||||||
Db        550 CGTGAAACAGCGTGCTGCACTGATCGACTGCCTGGCTCCGGATCGTCGCGTAGAGATCGA 491

Qy        993 AGTTAAAGGCTACAAAGAAGTTGTAACTCAGCCGGCGGGTTAA 1035
              |||||||||   |||||| ||||||||||||||  || ||||
Db        490 AGTTAAAGGTATCAAAGACGTTGTAACTCAGCCGCAGGCTTAA 448
```

RESULT 9
CF563206/c
LOCUS CF563206 323 bp mRNA linear EST 23-SEP-2003
DEFINITION 1115082A08.y1 C. reinhardtii CC-1690 (mt+), Stress III (normalized), Lambda Zap II Chlamydomonas reinhardtii cDNA 5', mRNA sequence.
ACCESSION CF563206
VERSION CF563206.1 GI:34989289
KEYWORDS EST.
SOURCE Chlamydomonas reinhardtii
ORGANISM Chlamydomonas reinhardtii
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales; Chlamydomonadaceae; Chlamydomonas.
REFERENCE 1 (bases 1 to 323)
AUTHORS Grossman,A., Chang,C.-W., Davies,J., Harris,E., Hauser,C., Merchant,S., Quinn,J. and Shrager,J.
TITLE Analyses of the Chlamydomonas reinhardtii Genome: A Model, Unicellular System for Analyzing Gene Function and Regulation in Vascular Plants. Project: 1115
JOURNAL Unpublished (2003)
COMMENT Contact: Charles Hauser
DCMB Box 91000
Duke University
Durham, NC 27708-1000
Tel: 919 613 8159
Fax: 919 613 8177
Email: chauser@duke.edu
High quality sequence stop: 323.
FEATURES Location/Qualifiers
source 1. .323
/organism="Chlamydomonas reinhardtii"
/mol_type="mRNA"
/strain="CC-1690 wild type mt+ 21gr"
/db_xref="taxon:3055"
/clone_lib="C. reinhardtii CC-1690 (mt+), Stress III (normalized), Lambda Zap II"
/note="Vector: pBluescript II SK-; Site_1: EcoRI; Site_2: XhoI; Stress condition III library, constructed by Jeanette Quinn and Chiung-Wen Chang, combines cDNAs from CC-1690 cells grown to mid-log phase in copper-free TAP medium (see Quinn and Merchant(1998) Methods in Enzymology, 2997:263-279)in a shaking(250 rpm) illuminated (about 100 micromole/m2/sec) incubator at 22 C (see Quinn and Merchant(1998) Methods in Enzymology, 2997:263-279); CC-1690 cells grown to mid-log phase in low Fe (1 micromolar Fe) TAP medium (see La Fontaine S, Quinn JM, Nakamoto SS, Page MD, Gohre V, Moseley JL, Kropat J, Merchant S.LaFontaine et al. (2002) Eukaryotic Cell, 1:736-757) in a shaking illuminated incubator (same conditions as above). CC-1690 cells were grown to mid-log phase in TAP medium in a shaking illuminated incubator to

a density of 8x10e6 cells/ml. The flask was transferred to a shaking platform (200 rpm) at room temperature (23C) 12 micromole/m2/sec illumination and bubbled in a stoppered flask with 98% nitrogen, 2% CO2 gas mixture for 1 hour prior to harvesting for RNA isolation (as per Quinn JM, Barraco P, Eriksson M, Merchant S. Quinn et al. (2000) JBC 275:6080-6089); CC-1690 cells grown to mid-log phase (3x10e6 cells/ml) in TAP medium in a shaking (150 rpm) illuminated (70 mole photon/m2/sec) incubator at 27 C. Cells were diluted to 1x10e6 cells/ml, transferred to high light (11000 mol photon/m2/s) with shaking (150 rpm) and sampled at (0.5, 1,2,4,6, 12 hrs); CC-1690 cells grown to mid-log phase in HS medium in a shaking (150 rpm) illuminated (70 mole photon/m2/sec) incubator at 27 C. Cells were diluted to 1x10e6 cells/ml, transferred to high light (11000 mol photon/m2/s) with shaking (150 rpm) and sampled at (0.5, 1,2,4,6, 12 hrs). PolyA mRNA was purified from each sample, pooled and cDNA synthesized (see Shrager et al, Plant Physiol. 131, 401-408 for details). The cDNA was directionally cloned into lambda Zap II (Stratagene) in the EcoRI (5') and XhoRI (3') sites. pBluescript II SK- plasmids were excised from the lambda ZAP clones by superinfection with ExAssist (Stratagene) phage. The library was normalized using method 4 described in Bonaldo et al., (1996) Genome Research 6: 791-806."

ORIGIN

Query Match 17.0%; Score 176; DB 7; Length 323;
Best Local Similarity 84.9%; Pred. No. 3.1e-40;
Matches 197; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

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Qy        804 CCAGCAGCTGTCTGAGAAACGTGCTCAGTCCGTTGTTGACTACCTGGTTGCTAAAGGCAT 863
              ||||   |||||  |||   |||||||||| ||||||| ||||||  |   | |||||  ||
Db        323 CCAGGGTCTGTCCGAGCGCCGTGCTCAGTCTGTTGTTGATTACCTGATCTCCAAAGGTAT 264

Qy        864 CCCGGCTGGCAAAATCTCCGCTCGCGGCATGGGTGAATCCAACCCGGTTACTGGCAACAC 923
              ||||||  | |||  |||||||| ||  ||  ||||| ||||||||||||||||||||||||
Db        263 CCCGGCAGACAAGATCTCCGCACGTGGTATGGGCGAATCCAACCCGGTTACTGGCAACAC 204

Qy        924 CTGTGACAACGTGAAAGCTCGCGCTGCCCTGATCGATTGCCTGGCTCCGGATCGTCGTGT 983
              ||||||||||||||||   || |||||  |||||||| ||||||||||||||||||||  ||
Db        203 CTGTGACAACGTGAAACAGCGTGCTGCACTGATCGACTGCCTGGCTCCGGATCGTCGCGT 144

Qy        984 AGAGATCGAAGTTAAAGGCTACAAAGAAGTTGTAACTCAGCCGGCGGGTTAA 1035
              ||||||||||||||||   ||||||  ||||||||||||||  || ||||
Db        143 AGAGATCGAAGTTAAAGGTATCAAAGACGTTGTAACTCAGCCGCAGGCTTAA 92
```

RESULT 10
BE423296
LOCUS BE423296 603 bp mRNA linear EST 24-JUL-2000
DEFINITION WHE0063_E04_I07ZS Wheat endosperm cDNA library Triticum aestivum cDNA clone WHE0063_E04_I07, mRNA sequence.
ACCESSION BE423296
VERSION BE423296.1 GI:9421139
KEYWORDS EST.
SOURCE Triticum aestivum (bread wheat)
ORGANISM Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Triticum.
REFERENCE 1 (bases 1 to 603)
AUTHORS Altenbach,S., Anderson,O.D., Chao,S., Galili,G., Han,P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Miller,R., Rausch,C.J., Seaton,C.L. and Tong,J.C.
TITLE The structure and function of the expressed portion of the wheat genomes - Endosperm cDNA library
JOURNAL Unpublished (2000)
COMMENT Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
Fax: 5105595818
Email: oandersn@pw.usda.gov
Sequence have been trimmed to remove vector sequence and low quality sequence with phred score less than 20
Seq primer: Stratagene SK primer.
FEATURES Location/Qualifiers
source 1. .603
/organism="Triticum aestivum"
/mol_type="mRNA"
/cultivar="Cheyenne"
/db_xref="taxon:4565"
/clone="WHE0063_E04_I07"
/tissue_type="Endosperm"
/dev_stage="5 to 30 days post anthesis seed"
/lab_host="E. coli SOLR"
/clone_lib="Wheat endosperm cDNA library"
/note="Vector: Lambda ZAP II, excised phagemid; Site_1: EcoRI; Seeds collected, endosperm isolated, and RNA prepared by Susan Altenbach. Library constructed by Stratagene, Inc. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab."
ORIGIN

Query Match 15.4%; Score 159; DB 2; Length 603;
Best Local Similarity 77.9%; Pred. No. 3.6e-35;
Matches 211; Conservative 0; Mismatches 45; Indels 15; Gaps 1;

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Qy        200 TGGGTTATGACTGGCTGGGCCGTATGGCATATAAAGGCAGCGTTGACAACGGTGCTTTCA 259
              |||||| |||||| | || |||||| | || |||||||||||||| |||||||| | ||
Db        149 TGGGTTACGACTGGTTAGGTCGTATGCCGTACAAAGGCAGCGTTGAAAACGGTGCATACA 208

Qy        260 AAGCTCAGGGCGTTCAGCTGACCGCTAAACTGGGTTACCCGATCACTGACGATCTGGACA 319
              |||||||||||||||| |||||||||||||||||||||||| |||||||||| |||||||
Db        209 AAGCTCAGGGCGTTCAACTGACCGCTAAACTGGGTTACCCAATCACTGACGACCTGGACA 268

Qy        320 TCTACACCCGTCTGGGCGGCATGGTTTGGCGCGCTGACTCCAAAGGCAACTACGCTTCTA 379
              ||||||| |||||||| |||||||| ||||| || ||| | |||  |||
Db        269 TCTACACTCGTCTGGGTGGCATGGTATGGCGTGCAGACACTAAATCCAA---------- 317

Qy        380 CCGGCGTTTCCCGTAGCGAACACGACACTGGCGTTTCCCCAGTATTTGCTGGCGGCGTAG 439
                  |||||   |||   | |||||||| |||||||| || || || |||||||| || |
Db        318 ----CGTTTATGGTAAAAACCACGACACCGGCGTTTCTCCGGTCTTCGCTGGCGGTGTTG 373

Qy        440 AGTGGGCTGTTACTCGTGACATCGCTACCCG 470
              |||  ||  | |||| ||| |||||  |||
Db        374 AGTACGCGATCACTCCTGAAATCGCTCGCCG 404
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RESULT 11
AF075794/c
LOCUS AF075794 655 bp DNA linear GSS 29-AUG-2000
DEFINITION AF075794 Salmonella typhimurium LT2, Lambda DASH II Salmonella typhimurium genomic clone 107-T3, genomic survey sequence.
ACCESSION AF075794
VERSION AF075794.1 GI:3320664
KEYWORDS GSS.
SOURCE Salmonella typhimurium
ORGANISM Salmonella typhimurium
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Salmonella.
REFERENCE 1 (bases 1 to 655)
AUTHORS Wong,R.M.-Y., Wong,K.K., Benson,N.R. and McClelland,M.
TITLE Sample sequencing of a Salmonella typhimurium LT2 lambda library: comparison to the Escherichia coli K12 genome
JOURNAL FEMS Microbiol. Lett. 173 (2), 411-423 (1999)
MEDLINE 99243757
PUBMED 10227170
COMMENT Contact: McClelland M
Molecular Biology
Sidney Kimmel Cancer Center
3099 Science Park Road, San Diego, CA 92121, USA
Email: mcclelland@lifsci.sdsu.edu
Class: shotgun.

```
FEATURES             Location/Qualifiers
     source          1. .655
                     /organism="Salmonella typhimurium"
                     /mol_type="genomic DNA"
                     /strain="LT2"
                     /db_xref="taxon:602"
                     /clone="107-T3"
                     /clone_lib="Salmonella typhimurium LT2, Lambda DASH II"
                     /note="Vector: Lambda DASH II; sequenced using Li-Cor
                     sequencer"
ORIGIN

  Query Match             13.0%;  Score 134.2;  DB 8;  Length 655;
  Best Local Similarity   72.7%;  Pred. No. 7.1e-28;
  Matches  194;  Conservative    0;  Mismatches   58;  Indels   15;  Gaps    1;

Qy          15 CGTACTGAATGCGGCTCCGAAAGATAACACCTGGTATGCAGGTGGTAAACTGGGTTGGTC 74
               ||||  | | || ||||||||||||||||||||||| || |||| ||||||||| |||||
Db         252 CGTAGCGCAGGCCGCTCCGAAAGATAACACCTGGTACGCTGGTGCTAAACTGGGCTGGTC 193

Qy          75 CCAGTATCACGACACCGGTTTCTACGGTAACGGTTTCCAGAACAACAACGGTCCGACCCG 134
                ||||| || |||||                ||| |||    ||||  | || ||||| |
Db         192 TCAGTACCATGACAC---------------CGGCTTCATTCACAATGATGGCCCGACTCA 148

Qy         135 TAACGATCAGCTTGGTGCTGGTGCGTTCGGTGGTTACCAGGTTAACCCGTACCTCGGTTT 194
               | |  |.|| || || || ||||| || |||||||||||||||||||  | || ||
Db         147 TGAAAACCAACTGGGCGCAGGTGCTTTTGGTGGTTACCAGGTTAACCCGTATGTTGGCTT 88

Qy         195 CGAAATGGGTTATGACTGGCTGGGCCGTATGGCATATAAAGGCAGCGTTGACAACGGTGC 254
               |||||||| || |||||| | ||||||||| | || ||||||  |     ||| || ||
Db          87 TGAAATGGGCTACGACTGGTTAGGCCGTATGCCGTACAAAGGCGACTACATCAATGGCGC 28

Qy         255 TTTCAAAGCTCAGGGCGTTCAGCTGAC 281
               ||  ||||||||| ||||||||| ||||
Db          27 TTATAAAGCTCAGCGCGTTCAGTTGAC 1


RESULT 12
CF915072
LOCUS       CF915072                601 bp    mRNA    linear   EST 05-NOV-2003
DEFINITION  B0973F11-5 NIA Mouse Unfertilized Egg cDNA Library (Long 1) Mus
            musculus cDNA clone NIA:B0973F11 IMAGE:30479302 5', mRNA sequence.
ACCESSION   CF915072
VERSION     CF915072.1  GI:38186274
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 601)
  AUTHORS   Piao,Y., Ko,N.T., Lim,M.K. and Ko,M.S.H.
  TITLE     Construction of long-transcript enriched cDNA libraries from
            submicrogram amounts of total RNAs by a universal PCR amplification
            method
  JOURNAL   Genome Res. 11 (9), 1553-1558 (2001)
  MEDLINE   21429098
   PUBMED   11544199
COMMENT     Contact: Dawood B. Dudekula
            Laboratory of Genetics
            National Institute on Aging/National Institutes of Health
            333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
            Email: cdna@lgsun.grc.nia.nih.gov
            Plate: B0973  row: F  column: 11
            Seq primer: M13 Reverse
            High quality sequence stop: 601
            POLYA=No.
FEATURES             Location/Qualifiers
     source          1. .601
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6J"
                     /db_xref="niaEST:B0973F11-5"
                     /db_xref="taxon:10090"
                     /clone="NIA:B0973F11 IMAGE:30479302"
                     /dev_stage="Unfertilized Egg"
                     /lab_host="DH10B"
                     /clone_lib="NIA Mouse Unfertilized Egg cDNA Library (Long
                     1)"
                     /note="Vector: pCMV-SPORT6 (Invitrogen); Site_1: SalI;
                     Site_2: NotI; Mouse cDNA project by the Laboratory of
                     Genetics, National Institute on Aging (NIA), Intramural
                     Research Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA).
                     This is a long-transcript enriched cDNA library (Ref.
                     Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). Total
                     RNAs were extracted from a pool of 1488 unfertilized eggs.
                     Double-stranded cDNAs were synthesized with an Oligo(dT)
                     primer [Invitrogen:
                     5'-pGACTAGTTCTAGATCGCGAGCGGCCGCCCTTTTTTTTTTTTTTT-3'],
                     treated with T4 DNA polymerase, and purified by
                     ethanol-precipitation. The cDNAs were ligated to
                     Lone-linker LL-Sal4, purified by phenol/chloroform, and
                     separated from free linkers by Centricon 100. Then, the
                     cDNAs were amplified by long-range high fidelity PCR using
                     Ex Taq polymerase (Takara) with a primer Sal4-S. The
                     products were purified by phenol/chloroform and Centricon
                     100. The cDNAs were digested with SalI and NotI enzymes
                     and cloned into SalI/NotI site of pCMV-SPORT6 plasmid
                     vector. The DH10B E. coli host was transformed with the
                     ligation mixture by the standard chemical method. The
                     average insert size is about 2.5 kb. The library was
                     constructed by Yulan Piao."
ORIGIN

  Query Match             5.9%;  Score 61.4;  DB 7;  Length 601;
  Best Local Similarity   59.4%;  Pred. No. 1.6e-06;
  Matches  104;  Conservative    0;  Mismatches   71;  Indels    0;  Gaps    0;

Qy         755 CCGCTGTTGTTCTGGGCTACACCGACCGCATCGGTTCCGAAGCTTACAACCAGCAGCTGT 814
               || | ||||||   ||  |||| |||  | ||||| | || |||||||||||| ||||||
Db         339 CCACCGTTGTTGAAGGTCACACTGACTCCGTCGGTCCTGACGCTTACAACCAGAAGCTGT 398

Qy         815 CTGAGAAACGTGCTCAGTCCGTTGTTGACTACCTGGTTGCTAAAGGCATCCCGGCTGGCA 874
               |  ||   |||||| |  | |||     |   ||||||      | || ||  |  ||  |
Db         399 CCCAGCGTCGTGCTGACGCTGTTAAGCAAGTCCTGGTCAAAGACGGTATTGCTCCTAACC 458

Qy         875 AAATCTCCGCTCGCGGCATGGGTGAATCCAACCCGGTTACTGGCAACACCTGTGA 929
                  |  | |    ||    ||  ||||| ||| ||| ||| |||| |   |||
Db         459 GTGTAAGCTCGGTTGGTTATGGCAAATCCCGCCCAGTTGCTGACAACGCAACTGA 513


RESULT 13
CF915603
LOCUS       CF915603                601 bp    mRNA    linear   EST 05-NOV-2003
DEFINITION  B0982E05-5 NIA Mouse Unfertilized Egg cDNA Library (Long 1) Mus
            musculus cDNA clone NIA:B0982E05 IMAGE:30480148 5', mRNA sequence.
ACCESSION   CF915603
VERSION     CF915603.1  GI:38186805
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 601)
  AUTHORS   Piao,Y., Ko,N.T., Lim,M.K. and Ko,M.S.H.
  TITLE     Construction of long-transcript enriched cDNA libraries from
            submicrogram amounts of total RNAs by a universal PCR amplification
            method
  JOURNAL   Genome Res. 11 (9), 1553-1558 (2001)
  MEDLINE   21429098
   PUBMED   11544199
COMMENT     Contact: Dawood B. Dudekula
            Laboratory of Genetics
            National Institute on Aging/National Institutes of Health
            333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
            Email: cdna@lgsun.grc.nia.nih.gov
            Plate: B0982  row: E  column: 05
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            Seq primer: M13 Reverse
            High quality sequence stop: 601
            POLYA=No.
FEATURES              Location/Qualifiers
     source           1. .601
                      /organism="Mus musculus"
                      /mol_type="mRNA"
                      /strain="C57BL/6J"
                      /db_xref="niaEST:B0982E05-5"
                      /db_xref="taxon:10090"
                      /clone="NIA:B0982E05 IMAGE:30480148"
                      /dev_stage="Unfertilized Egg"
                      /lab_host="DH10B"
                      /clone_lib="NIA Mouse Unfertilized Egg cDNA Library (Long
                      1)"
                      /note="Vector: pCMV-SPORT6 (Invitrogen); Site_1: SalI;
                      Site_2: NotI; Mouse cDNA project by the Laboratory of
                      Genetics, National Institute on Aging (NIA), Intramural
                      Research Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA).
                      This is a long-transcript enriched cDNA library (Ref.
                      Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). Total
                      RNAs were extracted from a pool of 1488 unfertilized eggs.
                      Double-stranded cDNAs were synthesized with an Oligo(dT)
                      primer [Invitrogen:
                      5'-pGACTAGTTCTAGATCGCGAGCGGCCGCCCTTTTTTTTTTTTTTT-3'],
                      treated with T4 DNA polymerase, and purified by
                      ethanol-precipitation. The cDNAs were ligated to
                      Lone-linker LL-Sal4, purified by phenol/chloroform, and
                      separated from free linkers by Centricon 100. Then, the
                      cDNAs were amplified by long-range high fidelity PCR using
                      Ex Taq polymerase (Takara) with a primer Sal4-S. The
                      products were purified by phenol/chloroform and Centricon
                      100. The cDNAs were digested with SalI and NotI enzymes
                      and cloned into SalI/NotI site of pCMV-SPORT6 plasmid
                      vector. The DH10B E. coli host was transformed with the
                      ligation mixture by the standard chemical method. The
                      average insert size is about 2.5 kb. The library was
                      constructed by Yulan Piao."
ORIGIN

  Query Match             5.9%;  Score 61.4;  DB 7;  Length 601;
  Best Local Similarity   59.4%;  Pred. No. 1.6e-06;
  Matches  104;  Conservative    0;  Mismatches   71;  Indels    0;  Gaps    0;

Qy        755 CCGCTGTTGTTCTGGGCTACACCGACCGCATCGGTTCCGAAGCTTACAACCAGCAGCTGT 814
              || | ||||||   ||  |||| |||  | ||||| | || ||||||||||||| ||||||
Db        339 CCACCGTTGTTGAAGGTCACACTGACTCCGTCGGTCCTGACGCTTACAACCAGAAGCTGT 398

Qy        815 CTGAGAAACGTGCTCAGTCCGTTGTTGACTACCTGGTTGCTAAAGGCATCCCGGCTGGCA 874
              |  ||   |||||| |  | |||   |  ||||||     | || ||  |  ||  |
Db        399 CCCAGCGTCGTGCTGACGCTGTTAAGCAAGTCCTGGTCAAAGACGGTATTGCTCCTAACC 458

Qy        875 AAATCTCCGCTCGCGGCATGGGTGAATCCAACCCGGTTACTGGCAACACCTGTGA 929
              |   | |    ||    ||  |||||  ||| ||| ||| |||| |   |||
Db        459 GTGTAAGCTCGGTTGGTTATGGCAAATCCCGCCCAGTTGCTGACAACGCAACTGA 513


RESULT 14
CF544559
LOCUS       CF544559                736 bp    mRNA    linear   EST 01-OCT-2003
DEFINITION  Hd_mx17_67B10_T7 Hypsibius dujardini mixed stage (fraction 7)
            Hypsibius dujardini cDNA clone Hd_mx17_67B10 5' similar to Q52465
            (Q52465) Protein F precursor (Fragment), mRNA sequence.
ACCESSION   CF544559
VERSION     CF544559.1  GI:37213423
KEYWORDS    EST.
SOURCE      Hypsibius dujardini
  ORGANISM  Hypsibius dujardini
            Eukaryota; Metazoa; Tardigrada; Eutardigrada; Apochela;
            Hypsibiidae; Hypsibius.
REFERENCE   1  (bases 1 to 736)
  AUTHORS   Daub,J., Thomas,F., Aboobaker,A. and Blaxter,M.L.
  TITLE     A survey of genes expressed in the tardigrade Hypsibius dujardini
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Blaxter ML
            Institute of Cell, Animal and Population Biology
            University of Edinburgh
            Ashworth Labs, King's Buildings, West Mains Road, Edinburgh, EH9
            3JT, UK.
            Tel: +44 131 650 6760
            Fax: +44 131 670 5450
            Email: mark.blaxter@ed.ac.uk
            The library was constructed from mixed stages of the tardigrade
            Hypsibius dujardini maintained in lab culture. The original source
            culture was obtained from Sciento (strain Z151). The library was
            constructed by Jennifer Daub, University of Edinburgh. Sequencing
            was performed by Frances Thomas, University of Edinburgh.
            PCR PRimers
            FORWARD: M13R
            BACKWARD: M13L
            Plate: 67  row: B  column: 10
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            High quality sequence stop: 533.
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                      /mol_type="mRNA"
                      /db_xref="taxon:232323"
                      /clone="Hd_mx17_67B10"
                      /sex="parthenogenic"
                      /tissue_type="whole body"
                      /dev_stage="mixed (adult and juvenile)"
                      /clone_lib="Hypsibius dujardini mixed stage (fraction 7)"
                      /note="Vector: pSPORT1; Site_1: Sal I (5'end); Site_2: Not
                      I (3'end); Tardigrades (also know as water bears) are
                      small free living animals inhabiting marine, fresh water
                      and water film habitats. Hypsibius dujardini is a
                      freshwater species maintained in lab culture. The library
                      was prepared from adults and juveniles and was constructed
                      by Jennifer Daub, University of Edinburgh."
ORIGIN

  Query Match             5.9%;  Score 61.4;  DB 7;  Length 736;
  Best Local Similarity   59.4%;  Pred. No. 1.7e-06;
  Matches  104;  Conservative    0;  Mismatches   71;  Indels    0;  Gaps    0;

Qy        755 CCGCTGTTGTTCTGGGCTACACCGACCGCATCGGTTCCGAAGCTTACAACCAGCAGCTGT 814
              || | ||||||   ||  |||| |||  | ||||| | || ||||||||||||| ||||||
Db        357 CCACCGTTGTTGAAGGTCACACTGACTCCGTCGGTCCTGACGCTTACAACCAGAAGCTGT 416

Qy        815 CTGAGAAACGTGCTCAGTCCGTTGTTGACTACCTGGTTGCTAAAGGCATCCCGGCTGGCA 874
              |  ||   |||||| |  | |||   |  ||||||     | || ||  |  ||  |
Db        417 CCCAGCGTCGTGCTGACGCTGTTAAGCAAGTCCTGGTCAAAGACGGTATTGCTCCTAACC 476

Qy        875 AAATCTCCGCTCGCGGCATGGGTGAATCCAACCCGGTTACTGGCAACACCTGTGA 929
              |   | |    ||    ||  |||||  ||| ||| ||| |||| |   |||
Db        477 GTGTAAGCTCGGTTGGTTATGGCAAATCCCGCCCAGTTGCTGACAACGCAACTGA 531


RESULT 15
CK326686
LOCUS       CK326686                763 bp    mRNA    linear   EST 17-DEC-2003
DEFINITION  Hd_mx24_02F09_T7 Hypsibius dujardini mixed stage 5'capped (fraction
            4) Hypsibius dujardini cDNA clone Hd_mx24_02F09 5' similar to
            Q52465 (Q52465) Protein F precursor (Fragment), mRNA sequence.
ACCESSION   CK326686
VERSION     CK326686.1  GI:40006296
KEYWORDS    EST.
SOURCE      Hypsibius dujardini
  ORGANISM  Hypsibius dujardini
            Eukaryota; Metazoa; Tardigrada; Eutardigrada; Apochela;
            Hypsibiidae; Hypsibius.
REFERENCE   1  (bases 1 to 763)
  AUTHORS   Daub,J., Thomas,F., Aboobaker,A. and Blaxter,M.L.
  TITLE     A survey of genes expressed in the tardigrade Hypsibius dujardini
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  JOURNAL   Unpublished (2003)
COMMENT     Contact: Blaxter ML
            Institute of Cell, Animal and Population Biology
            University of Edinburgh
            Ashworth Labs, King's Buildings, West Mains Road, Edinburgh, EH9
            3JT, UK.
            Tel: +44 131 650 6760
            Fax: +44 131 670 5450
            Email: mark.blaxter@ed.ac.uk
            PCR PRimers
            FORWARD: M13R
            BACKWARD: M13L
            Plate: 02  row: F  column: 09
            Seq primer: T7 (TAATACGACTCACTATAGGG)
            High quality sequence stop: 542.
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                     /clone_lib="Hypsibius dujardini mixed stage 5'capped
                     (fraction 4)"
                     /note="Vector: pSPORT1; Site_1: Sal I (5'end); Site_2: Not
                     I (3'end); Tardigrades (also know as water bears) are
                     small free living animals inhabiting marine, fresh water
                     and water film habitats. Hypsibius dujardini is a
                     freshwater species maintained in lab culture (source
                     strain Sciento Z151). The library was prepared from adults
                     and juveniles and was constructed in pSPORT1 vector
                     (Superscript, Invitrogen) using GeneRacer (Invitrogen)
                     purified 5'capped mRNA by Jennifer Daub, University of
                     Edinburgh. Sequencing was performed by Frances Thomas,
                     University of Edinburgh."
ORIGIN

  Query Match             5.9%;  Score 61.4;  DB 7;  Length 763;
  Best Local Similarity   59.4%;  Pred. No. 1.7e-06;
  Matches  104;  Conservative    0;  Mismatches   71;  Indels    0;  Gaps    0;

Qy        755 CCGCTGTTGTTCTGGGCTACACCGACCGCATCGGTTCCGAAGCTTACAACCAGCAGCTGT 814
              || | ||||||   ||  |||| |||  | ||||| | || ||||||||||||| ||||||
Db        356 CCACCGTTGTTGAAGGTCACACTGACTCCGTCGGTCCTGACGCTTACAACCAGAAGCTGT 415

Qy        815 CTGAGAAACGTGCTCAGTCCGTTGTTGACTACCTGGTTGCTAAAGGCATCCCGGCTGGCA 874
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Db        416 CCCAGCGTCGTGCTGACGCTGTTAAGCAAGTCCTGGTCAAAGACGGTATTGCTCCTAACC 475

Qy        875 AAATCTCCGCTCGCGGCATGGGTGAATCCAACCCGGTTACTGGCAACACCTGTGA 929
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Search completed: January 19, 2005, 16:36:47
Job time : 3915 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: January 19, 2005, 15:31:38 ; Search time 669 Seconds
(without alignments)
8889.379 Million cell updates/sec

Title: US-09-913-772-1
Perfect score: 1035
Sequence: 1 atgaaagcaatttтcgtact.....taactcagccggcgggttaa 1035

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4300275 seqs, 2872944193 residues

Total number of hits satisfying chosen parameters: 8600550

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*
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2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1035	100.0	1035	14	US-10-169-953-1	Sequence 1, Appli
2	1008	97.4	1008	14	US-10-091-257-13	Sequence 13, Appl
3	724.4	70.0	730	9	US-09-452-599-11	Sequence 11, Appl
4	724.4	70.0	730	15	US-10-121-120-11	Sequence 11, Appl
5	696.2	67.3	1422	18	US-10-425-821-69	Sequence 69, Appl
6	403	38.9	411	16	US-10-432-056-1	Sequence 1, Appli
7	303.4	29.3	3630	17	US-10-416-708A-23	Sequence 23, Appl
8	300.6	29.0	3603	17	US-10-416-708A-26	Sequence 26, Appl
9	298.6	28.9	3660	17	US-10-416-708A-9	Sequence 9, Appli
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11	219	21.2	3817	15	US-10-033-399B-24	Sequence 24, Appl
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13	161	15.6	1095	18	US-10-854-299-150	Sequence 150, App
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26	125.4	12.1	1035	15	US-10-336-840-18	Sequence 18, Appl
27	125.4	12.1	1035	15	US-10-336-840-24	Sequence 24, Appl
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31	117.2	11.3	1026	15	US-10-336-840-22	Sequence 22, Appl
32	117.2	11.3	1026	15	US-10-336-840-25	Sequence 25, Appl
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38	44.8	4.3	687	16	US-10-282-122A-33267	Sequence 33267, A
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40	41.8	4.0	1395	15	US-10-369-493-35123	Sequence 35123, A
41	41.8	4.0	1395	15	US-10-369-493-38184	Sequence 38184, A
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43	40.6	3.9	1439	15	US-10-193-002-162	Sequence 162, App
44	40.6	3.9	1439	15	US-10-084-843-167	Sequence 167, App
45	40.2	3.9	678	15	US-10-156-761-3232	Sequence 3232, Ap

ALIGNMENTS

RESULT 1
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; Sequence 1, Application US/10169953
; Publication No. US20030044915A1
; GENERAL INFORMATION:
; APPLICANT: Thierry BAUSSANT
; APPLICANT: Pascale JEANNIN
; APPLICANT: Yves DELNESTE
; APPLICANT: FranOois LAWNY
; APPLICANT: Jean-Yves BONNEFOY
; TITLE OF INVENTION: METHOD FOR PREPARING A POLYPEPTIDE SOLUBLE IN AN AQUEOUS SOLVENT
; TITLE OF INVENTION: IN THE ABSENCE OF DETERGENT
; FILE REFERENCE: D18390
; CURRENT APPLICATION NUMBER: US/10/169,953
; CURRENT FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: FR 00 00070
; PRIOR FILING DATE: 2000-01-04
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1035
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1032)
; FEATURE:
; OTHER INFORMATION: P40
US-10-169-953-1

Query Match 100.0%; Score 1035; DB 14; Length 1035;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
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; Sequence 13, Application US/10091257
; Publication No. US20030064078A1
;   GENERAL INFORMATION:
;        APPLICANT: Binz, Hans
;                   N'Guyen, Ngoc Thien
;                   Baussant, Thierry
;                   Trudel, Michel
;        TITLE OF INVENTION: PEPTIDE FRAGMENT OF RESPIRATORY
;                            SYNCYTIAL VIRUS PROTEIN G, IMMUNOGENIC AGENT,PHARMACEUTICAL
;                            COMPOSITION CONTAINING IT AND PREPARATION PROCESS
;        NUMBER OF SEQUENCES: 75
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Gordon W. Hueschen
;             STREET: 715 The "H" Bldg., 310 East Michigan
;                     Avenue
;             CITY: Kalamazoo
;             STATE: MI
;             COUNTRY: USA
;             ZIP: 49007
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;                       (EPO)
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/091,257
;             FILING DATE: 05-Mar-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/721,979A
;             FILING DATE: October 4, 1996
;             APPLICATION NUMBER: FR 94 04009
;             FILING DATE: 06-APR-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Hueschen, Gordon W.
;             REGISTRATION NUMBER: 16,157
;             REFERENCE/DOCKET NUMBER: PF57PCTUS/dln
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 616-382-0030
;             TELEFAX: 616-382-2030
;   INFORMATION FOR SEQ ID NO: 13:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 1008 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: peptide
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;             LOCATION: 1..1008
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US-10-091-257-13

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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCACTGTGGGTACCCGTCCTGATAACGGCATGCTGAGCCTGGGCGTTTCCTACCGCTTC 540

Qy        568 GGTCAGGAAGATGCTGCACCGGTTGTTGCTCCGGCTCCGGCTCCGGCTCCGGAAGTGGCT 627
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GGTCAGGAAGATGCTGCACCGGTTGTTGCTCCGGCTCCGGCTCCGGCTCCGGAAGTGGCT 600

Qy        628 ACCAAGCACTTCACCCTGAAGTCTGACGTTCTGTTCAACTTCAACAAAGCTACCCTGAAA 687
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 ACCAAGCACTTCACCCTGAAGTCTGACGTTCTGTTCAACTTCAACAAAGCTACCCTGAAA 660

Qy        688 CCGGAAGGTCAGCAGGCTCTGGATCAGCTGTACACTCAGCTGAGCAACATGGATCCGAAA 747
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CCGGAAGGTCAGCAGGCTCTGGATCAGCTGTACACTCAGCTGAGCAACATGGATCCGAAA 720

Qy        748 GACGGTTCCGCTGTTGTTCTGGGCTACACCGACCGCATCGGTTCCGAAGCTTACAACCAG 807
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GACGGTTCCGCTGTTGTTCTGGGCTACACCGACCGCATCGGTTCCGAAGCTTACAACCAG 780

Qy        808 CAGCTGTCTGAGAAACGTGCTCAGTCCGTTGTTGACTACCTGGTTGCTAAAGGCATCCCG 867
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CAGCTGTCTGAGAAACGTGCTCAGTCCGTTGTTGACTACCTGGTTGCTAAAGGCATCCCG 840

Qy        868 GCTGGCAAAATCTCCGCTCGCGGCATGGGTGAATCCAACCCGGTTACTGGCAACACCTGT 927
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GCTGGCAAAATCTCCGCTCGCGGCATGGGTGAATCCAACCCGGTTACTGGCAACACCTGT 900

Qy        928 GACAACGTGAAAGCTCGCGCTGCCCTGATCGATTGCCTGGCTCCGGATCGTCGTGTAGAG 987
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GACAACGTGAAAGCTCGCGCTGCCCTGATCGATTGCCTGGCTCCGGATCGTCGTGTAGAG 960

Qy        988 ATCGAAGTTAAAGGCTACAAAGAAGTTGTAACTCAGCCGGCGGGTTAA 1035
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 ATCGAAGTTAAAGGCTACAAAGAAGTTGTAACTCAGCCGGCGGGTTAA 1008
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RESULT 3
US-09-452-599-11
; Sequence 11, Application US/09452599
; Patent No. US20020055101A1
; GENERAL INFORMATION:
; APPLICANT: Bergeron, Michel G.
; APPLICANT: Ouellette, Marc
; APPLICANT: Roy, Paul H.
; TITLE OF INVENTION: Specific and Universal Probes and Amplification Primers
; TITLE OF INVENTION: to Rapidly Detect and Identify Common Bacterial
; TITLE OF INVENTION: Pathogens and Antibiotic Resistance Genes from Clinical
; TITLE OF INVENTION: Specimens for Routine Diagnosis in Micro
; FILE REFERENCE: 12287.31
; CURRENT APPLICATION NUMBER: US/09/452,599
; CURRENT FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: 08/526,840
; PRIOR FILING DATE: 1995-09-11
; PRIOR APPLICATION NUMBER: 08/304,732
; PRIOR FILING DATE: 1994-09-12
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
;   LENGTH: 730
;   TYPE: DNA
;   ORGANISM: Klebsiella pneumoniae
US-09-452-599-11

```
  Query Match             70.0%;  Score 724.4;  DB 9;  Length 730;
  Best Local Similarity   99.9%;  Pred. No. 5.4e-226;
  Matches  725;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        276 GCTGACCGCTAAACTGGGTTACCCGATCACTGACGATCTGGACATCTACACCCGTCTGGG 335
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GCTGACCGCTAAACTGGGTTACCCGATCACTGACGATCTGGACATCTACACCCGTCTGGG 60

Qy        336 CGGCATGGTTTGGCGCGCTGACTCCAAAGGCAACTACGCTTCTACCGGCGTTTCCCGTAG 395
              |||||||||||||||||||||||||||||||||||||||||| |||||||||||||||||
Db         61 CGGCATGGTTTGGCGCGCTGACTCCAAAGGCAACTACGCTTCAACCGGCGTTTCCCGTAG 120

Qy        396 CGAACACGACACTGGCGTTTCCCCAGTATTTGCTGGCGGCGTAGAGTGGGCTGTTACTCG 455
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CGAACACGACACTGGCGTTTCCCCAGTATTTGCTGGCGGCGTAGAGTGGGCTGTTACTCG 180

Qy        456 TGACATCGCTACCCGTCTGGAATACCAGTGGGTTAACAACATCGGCGACGCGGGCACTGT 515
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TGACATCGCTACCCGTCTGGAATACCAGTGGGTTAACAACATCGGCGACGCGGGCACTGT 240

Qy        516 GGGTACCCGTCCTGATAACGGCATGCTGAGCCTGGGCGTTTCCTACCGCTTCGGTCAGGA 575
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GGGTACCCGTCCTGATAACGGCATGCTGAGCCTGGGCGTTTCCTACCGCTTCGGTCAGGA 300

Qy        576 AGATGCTGCACCGGTTGTTGCTCCGGCTCCGGCTCCGGCTCCGGAAGTGGCTACCAAGCA 635
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AGATGCTGCACCGGTTGTTGCTCCGGCTCCGGCTCCGGCTCCGGAAGTGGCTACCAAGCA 360

Qy        636 CTTCACCCTGAAGTCTGACGTTCTGTTCAACTTCAACAAAGCTACCCTGAAACCGGAAGG 695
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CTTCACCCTGAAGTCTGACGTTCTGTTCAACTTCAACAAAGCTACCCTGAAACCGGAAGG 420

Qy        696 TCAGCAGGCTCTGGATCAGCTGTACACTCAGCTGAGCAACATGGATCCGAAAGACGGTTC 755
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCAGCAGGCTCTGGATCAGCTGTACACTCAGCTGAGCAACATGGATCCGAAAGACGGTTC 480

Qy        756 CGCTGTTGTTCTGGGCTACACCGACCGCATCGGTTCCGAAGCTTACAACCAGCAGCTGTC 815
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CGCTGTTGTTCTGGGCTACACCGACCGCATCGGTTCCGAAGCTTACAACCAGCAGCTGTC 540

Qy        816 TGAGAAACGTGCTCAGTCCGTTGTTGACTACCTGGTTGCTAAAGGCATCCCGGCTGGCAA 875
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TGAGAAACGTGCTCAGTCCGTTGTTGACTACCTGGTTGCTAAAGGCATCCCGGCTGGCAA 600

Qy        876 AATCTCCGCTCGCGGCATGGGTGAATCCAACCCGGTTACTGGCAACACCTGTGACAACGT 935
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AATCTCCGCTCGCGGCATGGGTGAATCCAACCCGGTTACTGGCAACACCTGTGACAACGT 660

Qy        936 GAAAGCTCGCGCTGCCCTGATCGATTGCCTGGCTCCGGATCGTCGTGTAGAGATCGAAGT 995
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GAAAGCTCGCGCTGCCCTGATCGATTGCCTGGCTCCGGATCGTCGTGTAGAGATCGAAGT 720

Qy        996 TAAAGG 1001
              ||||||
Db        721 TAAAGG 726
```

RESULT 4
US-10-121-120-11
; Sequence 11, Application US/10121120
; Publication No. US20030180733A1
; GENERAL INFORMATION:
; APPLICANT: Bergeron, Michel G.

```
; APPLICANT:  Ouellette, Marc
; APPLICANT:  Roy, Paul H.
; TITLE OF INVENTION: Specific and Universal Probes and Amplification
; TITLE OF INVENTION:  Primers
; TITLE OF INVENTION:  to Rapidly Detect and Identify Common Bacterial
; TITLE OF INVENTION:  Pathogens and Antibiotic Resistance Genes from Clinical
; TITLE OF INVENTION:  Specimens for Routine Diagnosis in Micro
; FILE REFERENCE: 12287.31
; CURRENT APPLICATION NUMBER: US/10/121,120
; CURRENT FILING DATE:  2002-04-11
; PRIOR APPLICATION NUMBER: 09/452,599
; PRIOR FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: 08/304,732
; PRIOR FILING DATE: 1994-09-12
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
;   LENGTH: 730
;   TYPE: DNA
;   ORGANISM: Klebsiella pneumoniae
US-10-121-120-11

  Query Match             70.0%;  Score 724.4;  DB 15;  Length 730;
  Best Local Similarity   99.9%;  Pred. No. 5.4e-226;
  Matches  725;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       276 GCTGACCGCTAAACTGGGTTACCCGATCACTGACGATCTGGACATCTACACCCGTCTGGG 335
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1 GCTGACCGCTAAACTGGGTTACCCGATCACTGACGATCTGGACATCTACACCCGTCTGGG 60

Qy       336 CGGCATGGTTTGGCGCGCTGACTCCAAAGGCAACTACGCTTCTACCGGCGTTTCCCGTAG 395
             |||||||||||||||||||||||||||||||||||||||||| |||||||||||||||||
Db        61 CGGCATGGTTTGGCGCGCTGACTCCAAAGGCAACTACGCTTCAACCGGCGTTTCCCGTAG 120

Qy       396 CGAACACGACACTGGCGTTTCCCCAGTATTTGCTGGCGGCGTAGAGTGGGCTGTTACTCG 455
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       121 CGAACACGACACTGGCGTTTCCCCAGTATTTGCTGGCGGCGTAGAGTGGGCTGTTACTCG 180

Qy       456 TGACATCGCTACCCGTCTGGAATACCAGTGGGTTAACAACATCGGCGACGCGGGCACTGT 515
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       181 TGACATCGCTACCCGTCTGGAATACCAGTGGGTTAACAACATCGGCGACGCGGGCACTGT 240

Qy       516 GGGTACCCGTCCTGATAACGGCATGCTGAGCCTGGGCGTTTCCTACCGCTTCGGTCAGGA 575
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       241 GGGTACCCGTCCTGATAACGGCATGCTGAGCCTGGGCGTTTCCTACCGCTTCGGTCAGGA 300

Qy       576 AGATGCTGCACCGGTTGTTGCTCCGGCTCCGGCTCCGGCTCCGGAAGTGGCTACCAAGCA 635
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       301 AGATGCTGCACCGGTTGTTGCTCCGGCTCCGGCTCCGGCTCCGGAAGTGGCTACCAAGCA 360

Qy       636 CTTCACCCTGAAGTCTGACGTTCTGTTCAACTTCAACAAAGCTACCCTGAAACCGGAAGG 695
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       361 CTTCACCCTGAAGTCTGACGTTCTGTTCAACTTCAACAAAGCTACCCTGAAACCGGAAGG 420

Qy       696 TCAGCAGGCTCTGGATCAGCTGTACACTCAGCTGAGCAACATGGATCCGAAAGACGGTTC 755
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       421 TCAGCAGGCTCTGGATCAGCTGTACACTCAGCTGAGCAACATGGATCCGAAAGACGGTTC 480

Qy       756 CGCTGTTGTTCTGGGCTACACCGACCGCATCGGTTCCGAAGCTTACAACCAGCAGCTGTC 815
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       481 CGCTGTTGTTCTGGGCTACACCGACCGCATCGGTTCCGAAGCTTACAACCAGCAGCTGTC 540

Qy       816 TGAGAAACGTGCTCAGTCCGTTGTTGACTACCTGGTTGCTAAAGGCATCCCGGCTGGCAA 875
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       541 TGAGAAACGTGCTCAGTCCGTTGTTGACTACCTGGTTGCTAAAGGCATCCCGGCTGGCAA 600

Qy       876 AATCTCCGCTCGCGGCATGGGTGAATCCAACCCGGTTACTGGCAACACCTGTGACAACGT 935
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       601 AATCTCCGCTCGCGGCATGGGTGAATCCAACCCGGTTACTGGCAACACCTGTGACAACGT 660

Qy       936 GAAAGCTCGCGCTGCCCTGATCGATTGCCTGGCTCCGGATCGTCGTGTAGAGATCGAAGT 995
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       661 GAAAGCTCGCGCTGCCCTGATCGATTGCCTGGCTCCGGATCGTCGTGTAGAGATCGAAGT 720

Qy       996 TAAAGG 1001
             ||||||
Db       721 TAAAGG 726


RESULT 5
US-10-425-821-69
; Sequence 69, Application US/10425821
; Publication No. US20040219530A1
; GENERAL INFORMATION:
;  APPLICANT: BROUSSEAU, Roland
;  APPLICANT:  HAREL, Jos,e
;  APPLICANT:  BEKAL, Sadjia
;  TITLE OF INVENTION: ARRAY AND USES THEREOF
;  FILE REFERENCE: 86369-3
;  CURRENT APPLICATION NUMBER: US/10/425,821
;  CURRENT FILING DATE:  2003-04-30
;  NUMBER OF SEQ ID NOS: 176
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 69
;  LENGTH: 1422
;  TYPE: DNA
;  ORGANISM: Escherichia coli
US-10-425-821-69

  Query Match             67.3%;  Score 696.2;  DB 18;  Length 1422;
  Best Local Similarity   82.1%;  Pred. No. 1.2e-216;
  Matches  838;  Conservative    0;  Mismatches  153;  Indels   30;  Gaps    2;

Qy        15 CGTACTGAATGCGGCTCCGAAAGATAACACCTGGTATGCAGGTGGTAAACTGGGTTGGTC 74
             ||||  | | || |||||||||||||||||||||||  | |||| ||||||||| |||||
Db       337 CGTAGCGCAGGCCGCTCCGAAAGATAACACCTGGTACACTGGTGCTAAACTGGGCTGGTC 396

Qy        75 CCAGTATCACGACACCGGTTTCTACGGTAACGGTTTCCAGAACAACAACGGTCCGACCCG 134
             |||||| || || ||||||  |               |||||||| || |||||||
Db       397 CCAGTACCATGATACTGGTTTCATC---------------AACAACAATGGCCCGACCCA 441

Qy       135 TAACGATCAGCTTGGTGCTGGTGCGTTCGGTGGTTACCAGGTTAACCCGTACCTCGGTTT 194
             | |  | || || || |||||||| || |||||||||||||||||||||||  | || ||
Db       442 TGAAAACCAACTGGGCGCTGGTGCTTTTGGTGGTTACCAGGTTAACCCGTATGTTGGCTT 501

Qy       195 CGAAATGGGTTATGACTGGCTGGGCCGTATGGCATATAAAGGCAGCGTTGACAACGGTGC 254
              ||||||||||| |||||| | || |||||| | || |||||||||||||| ||||||||
Db       502 TGAAATGGGTTACGACTGGTTAGGTCGTATGCCGTACAAAGGCAGCGTTGAAAACGGTGC 561

Qy       255 TTTCAAAGCTCAGGGCGTTCAGCTGACCGCTAAACTGGGTTACCCGATCACTGACGATCT 314
              | |||||||||||||||||| ||||||||||||||||||||||| ||||||||||| ||
Db       562 ATACAAAGCTCAGGGCGTTCAACTGACCGCTAAACTGGGTTACCCAATCACTGACGACCT 621

Qy       315 GGACATCTACACCCGTCTGGGCGGCATGGTTTGGCGCGCTGACTCCAAAGGCAACTACGC 374
             |||||||||||| |||||||| |||||||| ||||| || ||| | |||  |||
Db       622 GGACATCTACACTCGTCTGGGTGGCATGGTATGGCGTGCAGACACTAAATCCAA------ 675

Qy       375 TTCTACCGGCGTTTCCCGTAGCGAACACGACACTGGCGTTTCCCCAGTATTTGCTGGCGG 434
                      ||||||   |||   | ||||||||| |||||||||| ||| || || ||||||
Db       676 ---------CGTTTATGGTAAAAACCACGACACCGGCGTTTCTCCGGTCTTCGCTGGCGG 726

Qy       435 CGTAGAGTGGGCTGTTACTCGTGACATCGCTACCCGTCTGGAATACCAGTGGGTTAACAA 494
              || ||||  ||  | |||| ||| |||||||||||||||||||||||||||   |||||
Db       727 TGTTGAGTACGCGATCACTCCTGAAATCGCTACCCGTCTGGAATACCAGTGGACGAACAA 786

Qy       495 CATCGGCGACGCGGGCACTGTGGGTACCCGTCCTGATAACGGCATGCTGAGCCTGGGCGT 554
             |||||| ||||||   |||  | || ||||| ||| || | ||||||||||||||||||| ||
Db       787 CATCGGTGACGCACACACCATCGGCACTCGTCCGGACAACGGCATGCTGAGCCTGGGTGT 846

Qy       555 TTCCTACCGCTTCGGTCAGGAAGATGCTGCACCGGTTGTTGCTCCGGCTCCGGCTCCGGC 614
             ||||||||| ||||||||||  || || || || || |||||||||||||||| ||||||||
Db       847 TTCCTACCGTTTCGGTCAGGGCGAGGCAGCTCCAGTAGTTGCTCCGGCTCCAGCTCCGGC 906

Qy       615 TCCGGAAGTGGCTACCAAGCACTTCACCCTGAAGTCTGACGTTCTGTTCAACTTCAACAA 674
              ||||||||    |||||||||||||| ||||||||||||||||||||||||||||||||
Db       907 ACCGGAAGTACAGACCAAGCACTTCACTCTGAAGTCTGACGTTCTGTTCAACTTCAACAA 966
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Qy        675 AGCTACCCTGAAACCGGAAGGTCAGCAGGCTCTGGATCAGCTGTACACTCAGCTGAGCAA 734
              ||| ||||||||||||||||||||    |||||||||||||||||||  ||||||||||
Db        967 AGCAACCCTGAAACCGGAAGGTCAGGCTGCTCTGGATCAGCTGTACAGCCAGCTGAGCAA 1026

Qy        735 CATGGATCCGAAAGACGGTTCCGCTGTTGTTCTGGGCTACACCGACCGCATCGGTTCCGA 794
              | ||||||||||||||||||||  |||||||||| |||||||||||||||||||||| ||
Db       1027 CTTGGATCCGAAAGACGGTTCCGTAGTTGTTCTGGGTTACACCGACCGCATCGGTTCTGA 1086

Qy        795 AGCTTACAACCAGCAGCTGTCTGAGAAACGTGCTCAGTCCGTTGTTGACTACCTGGTTGC 854
              ||||||||||||   ||||| |||   |||||||||| ||||||| ||||||  |  |
Db       1087 CGCTTACAACCAGGGTCTGTCCGAGCGCCGTGCTCAGTCTGTTGTTGATTACCTGATCTC 1146

Qy        855 TAAAGGCATCCCGGCTGGCAAAATCTCCGCTCGCGGCATGGGTGAATCCAACCCGGTTAC 914
              |||||  |||||||| | ||| |||||||| || || ||||| ||||||||||||||||
Db       1147 CAAAGGTATCCCGGCAGACAAGATCTCCGCACGTGGTATGGGCGAATCCAACCCGGTTAC 1206

Qy        915 TGGCAACACCTGTGACAACGTGAAAGCTCGCGCTGCCCTGATCGATTGCCTGGCTCCGGA 974
              ||||||||||||||||||||||||   || ||||| |||||||| ||||||||||||||
Db       1207 TGGCAACACCTGTGACAACGTGAAACAGCGTGCTGCACTGATCGACTGCCTGGCTCCGGA 1266

Qy        975 TCGTCGTGTAGAGATCGAAGTTAAAGGCTACAAAGAAGTTGTAACTCAGCCGGCGGGTTA 1034
              ||||||  |||||||||||||||||||   ||||||  |||||||||||||||  || |||
Db       1267 TCGTCGCGTAGAGATCGAAGTTAAAGGTATCAAAGACGTTGTAACTCAGCCGCAGGCTTA 1326

Qy       1035 A 1035
              |
Db       1327 A 1327
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RESULT 6
US-10-432-056-1
; Sequence 1, Application US/10432056
; Publication No. US20040014661A1
; GENERAL INFORMATION:
; APPLICANT: GOETSCH, Liliane
; APPLICANT: HAEUW, Jean-Francois
; APPLICANT: ROBERT, Alain
; TITLE OF INVENTION: PERIPLASMIC DOMAIN OF AN ENTEROBACTERIUM OMP PROTEIN
; TITLE OF INVENTION: AND ITS USE AS CARRIER OR ADJUVANT
; FILE REFERENCE: 344 667 - US
; CURRENT APPLICATION NUMBER: US/10/432,056
; CURRENT FILING DATE: 2003-05-16
; PRIOR APPLICATION NUMBER: PCT/FR 01/03 596
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: FR 00/14 909
; PRIOR FILING DATE: 2000-11-17
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 411
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(411)
US-10-432-056-1

Query Match 38.9%; Score 403; DB 16; Length 411;
Best Local Similarity 98.8%; Pred. No. 5.8e-121;
Matches 406; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Qy        622 GTGGCTACCAAGCACTTCACCCTGAAGTCTGACGTTCTGTTCAACTTCAACAAAGCTACC 681
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GTGGCTACCAAGCACTTCACCCTGAAGTCTGACGTTCTGTTCAACTTCAACAAAGCTACC 60

Qy        682 CTGAAACCGGAAGGTCAGCAGGCTCTGGATCAGCTGTACACTCAGCTGAGCAACATGGAT 741
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CTGAAACCGGAAGGTCAGCAGGCTCTGGATCAGCTGTACACTCAGCTGAGCAACATGGAT 120

Qy        742 CCGAAAGACGGTTCCGCTGTTGTTCTGGGCTACACCGACCGCATCGGTTCCGAAGCTTAC 801
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CCGAAAGACGGTTCCGCTGTTGTTCTGGGCTACACCGACCGCATCGGTTCCGAAGCTTAC 180

Qy        802 AACCAGCAGCTGTCTGAGAAACGTGCTCAGTCCGTTGTTGACTACCTGGTTGCTAAAGGC 861
              ||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db        181 AACCAGCAGCTGTCTGAGAAACGTGCTCAGTCCGTCGTTGACTACCTGGTTGCTAAAGGC 240

Qy        862 ATCCCGGCTGGCAAAATCTCCGCTCGCGGCATGGGTGAATCCAACCCGGTTACTGGCAAC 921
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ATCCCGGCTGGCAAAATCTCCGCTCGCGGCATGGGTGAATCCAACCCGGTTACTGGCAAC 300

Qy        922 ACCTGTGACAACGTGAAAGCTCGCGCTGCCCTGATCGATTGCCTGGCTCCGGATCGTCGT 981
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ACCTGTGACAACGTGAAAGCTCGCGCTGCCCTGATCGATTGCCTGGCTCCGGATCGTCGT 360

Qy        982 GTAGAGATCGAAGTTAAAGGCTACAAAGAAGTTGTAACTCAGCCGGCGGGT 1032
              ||||||||||||||||||||||||||||||||||||||||||||||||||   || |
Db        361 GTAGAGATCGAAGTTAAAGGCTACAAAGAAGTTGTAACTCAGCCTCAGGCT 411
```

RESULT 7
US-10-416-708A-23
; Sequence 23, Application US/10416708A
; Publication No. US20040161753A1
; GENERAL INFORMATION:
; APPLICANT: Wise, John G.
; APPLICANT: Fromknecht, Katja
; TITLE OF INVENTION: CREATION AND IDENTIFICATION OF PROTEINS HAVING NEW DNA BINDING
; TITLE OF INVENTION: SPECIFICITIES
; FILE REFERENCE: 37779-0004
; CURRENT APPLICATION NUMBER: US/10/416,708A
; CURRENT FILING DATE: 2004-01-28
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 23
; LENGTH: 3630
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Plasmid derived from pComp containing a hexahisadine separator
; OTHER INFORMATION: gene
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(600)
; OTHER INFORMATION: pComp derived DNA
; FEATURE:
; NAME/KEY: misc_binding
; LOCATION: (6)..(23)
; OTHER INFORMATION: target binding sequence from cauliflower mosaic virus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (55)..(624)
; OTHER INFORMATION: ompA his tag fusion
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (601)..(624)
; OTHER INFORMATION: linker and histag
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (658)..(3630)
; OTHER INFORMATION: pComp derived DNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (688)..(1137)
; OTHER INFORMATION: lacZ' fragment
US-10-416-708A-23

Query Match 29.3%; Score 303.4; DB 17; Length 3630;
Best Local Similarity 74.3%; Pred. No. 5.1e-88;
Matches 423; Conservative 0; Mismatches 116; Indels 30; Gaps 2;

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Qy         15 CGTACTGAATGCGGCTCCGAAAGATAACACCTGGTATGCAGGTGGTAAACTGGGTTGGTC 74
              ||||  | | || |||||||||||||||||||||  | |||| |||||||||| |||||
Db        111 CGTAGCGCAGGCCGCTCCGAAAGATAACACCTGGTACACTGGTGCTAAACTGGGCTGGTC 170
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Qy          75 CCAGTATCACGACACCGGTTTCTACGGTAACGGTTTCCAGAACAACAACGGTCCGACCCG 134
               |||||| || ||||| ||||||  |               |||||||| || |||||||
Db         171 CCAGTACCATGACACTGGTTTCATC--------------AACAACAATGGCCCGACCCA 215

Qy         135 TAACGATCAGCTTGGTGCTGGTGCGTTCGGTGGTTACCAGGTTAACCCGTACCTCGGTTT 194
               | |  | || || || |||||||| || ||||||||||||||||||||||  | || ||
Db         216 TGAAAACCAACTGGGCGCTGGTGCTTTTGGTGGTTACCAGGTTAACCCGTATGTTGGCTT 275

Qy         195 CGAAATGGGTTATGACTGGCTGGGCCGTATGGCATATAAAGGCAGCGTTGACAACGGTGC 254
               |||||||||| |||||| | || |||||| | || ||||||||||||| ||||||||
Db         276 TGAAATGGGTTACGACTGGTTAGGTCGTATGCCGTACAAAGGCAGCGTTGAAAACGGTGC 335

Qy         255 TTTCAAAGCTCAGGGCGTTCAGCTGACCGCTAAACTGGGTTACCCGATCACTGACGATCT 314
               | |||||||||||||||||| |||||||||||||||||||||| |||||||||| ||
Db         336 ATACAAAGCTCAGGGCGTTCAACTGACCGCTAAACTGGGTTACCCAATCACTGACGACCT 395

Qy         315 GGACATCTACACCCGTCTGGGCGGCATGGTTTGGCGCGCTGACTCCAAAGGCAACTACGC 374
               |||||||||||| |||||||| |||||||| ||||| || ||| | |||  |||
Db         396 GGACATCTACACTCGTCTGGGTGGCATGGTATGGCGTGCAGACACTAAATCCAA------ 449

Qy         375 TTCTACCGGCGTTTCCCGTAGCGAACACGACACTGGCGTTTCCCCAGTATTTGCTGGCGG 434
                     |||||    |||   | |||||||| |||||||| || || || ||||||||
Db         450 ---------CGTTTATGGTAAAAACCACGACACCGGCGTTTCTCCGGTCTTCGCTGGCGG 500

Qy         435 CGTAGAGTGGGCTGTTACTCGTGACATCGCTACCCGTCTGGAATACCAGTGGGTTAACAA 494
               || ||||  ||  | |||| ||| ||||||||||||||||||||||||   |||||
Db         501 TGTTGAGTACGCGATCACTCCTGAAATCGCTACCCGTCTGGAATACCAGTGGACCAACAA 560

Qy         495 CATCGGCGACGCGGGCACTGTGGGTACCCGTCCTGATAACGGCATGCTGAGCCTGGGCGT 554
               |||||| |||||   |||  | || || ||||| || |||||     |     |
Db         561 CATCGGTGACGCACACACCATCGGCACTCGTCCGGACAACGGTGGCCATCATCATCATCA 620

Qy         555 TTCCTACCGCTTCGGTCAGGAAGATGCTG 583
               |  |||  ||  || | |  |||||| ||
Db         621 TCACTAAGGCGGCGATTATAAAGATGATG 649


RESULT 8
US-10-416-708A-26
; Sequence 26, Application US/10416708A
; Publication No. US20040161753A1
; GENERAL INFORMATION:
;  APPLICANT: Wise, John G.
;  APPLICANT:  Fromknecht, Katja
;  TITLE OF INVENTION: CREATION AND IDENTIFICATION OF PROTEINS HAVING NEW DNA BINDING
;  TITLE OF INVENTION:  SPECIFICITIES
;  FILE REFERENCE: 37779-0004
;  CURRENT APPLICATION NUMBER: US/10/416,708A
;  CURRENT FILING DATE:  2004-01-28
;  NUMBER OF SEQ ID NOS: 89
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 26
;   LENGTH: 3603
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Plasmid derived from pComp containing a flag tag separator gene
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(600)
;   OTHER INFORMATION: pComp derived DNA
;   FEATURE:
;   NAME/KEY: misc_binding
;   LOCATION: (6)..(23)
;   OTHER INFORMATION: target binding site
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (55)..(630)
;   OTHER INFORMATION: ompA flag tag fusion
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (600)..(630)
;   OTHER INFORMATION: linker flag tag
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (631)..(3603)
;   OTHER INFORMATION: pComp derived DNA
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (661)..(1110)
;   OTHER INFORMATION: lacZ' fragment
US-10-416-708A-26

  Query Match           29.0%;  Score 300.6;  DB 17;  Length 3603;
  Best Local Similarity   77.2%;  Pred. No. 4.2e-87;
  Matches  404;  Conservative    0;  Mismatches   89;  Indels   30;  Gaps    2;

Qy          15 CGTACTGAATGCGGCTCCGAAAGATAACACCTGGTATGCAGGTGGTAAACTGGGTTGGTC 74
               ||||  | | || |||||||||||||||||||||||  | |||| |||||||| |||||
Db         111 CGTAGCGCAGGCCGCTCCGAAAGATAACACCTGGTACACTGGTGCTAAACTGGGCTGGTC 170

Qy          75 CCAGTATCACGACACCGGTTTCTACGGTAACGGTTTCCAGAACAACAACGGTCCGACCCG 134
               |||||| || ||||| ||||||  |               |||||||| || |||||||
Db         171 CCAGTACCATGACACTGGTTTCATC--------------AACAACAATGGCCCGACCCA 215

Qy         135 TAACGATCAGCTTGGTGCTGGTGCGTTCGGTGGTTACCAGGTTAACCCGTACCTCGGTTT 194
               | |  | || || || |||||||| || ||||||||||||||||||||||  | || ||
Db         216 TGAAAACCAACTGGGCGCTGGTGCTTTTGGTGGTTACCAGGTTAACCCGTATGTTGGCTT 275

Qy         195 CGAAATGGGTTATGACTGGCTGGGCCGTATGGCATATAAAGGCAGCGTTGACAACGGTGC 254
               |||||||||| |||||| | || |||||| | || ||||||||||||| ||||||||
Db         276 TGAAATGGGTTACGACTGGTTAGGTCGTATGCCGTACAAAGGCAGCGTTGAAAACGGTGC 335

Qy         255 TTTCAAAGCTCAGGGCGTTCAGCTGACCGCTAAACTGGGTTACCCGATCACTGACGATCT 314
               | |||||||||||||||||| |||||||||||||||||||||| |||||||||| ||
Db         336 ATACAAAGCTCAGGGCGTTCAACTGACCGCTAAACTGGGTTACCCAATCACTGACGACCT 395

Qy         315 GGACATCTACACCCGTCTGGGCGGCATGGTTTGGCGCGCTGACTCCAAAGGCAACTACGC 374
               |||||||||||| |||||||| |||||||| ||||| || ||| | |||  |||
Db         396 GGACATCTACACTCGTCTGGGTGGCATGGTATGGCGTGCAGACACTAAATCCAA------ 449

Qy         375 TTCTACCGGCGTTTCCCGTAGCGAACACGACACTGGCGTTTCCCCAGTATTTGCTGGCGG 434
                     |||||    |||   | |||||||| |||||||| || || || ||||||||
Db         450 ---------CGTTTATGGTAAAAACCACGACACCGGCGTTTCTCCGGTCTTCGCTGGCGG 500

Qy         435 CGTAGAGTGGGCTGTTACTCGTGACATCGCTACCCGTCTGGAATACCAGTGGGTTAACAA 494
               || ||||  ||  | |||| ||| ||||||||||||||||||||||||   |||||
Db         501 TGTTGAGTACGCGATCACTCCTGAAATCGCTACCCGTCTGGAATACCAGTGGACCAACAA 560

Qy         495 CATCGGCGACGCGGGCACTGTGGGTACCCGTCCTGATAACGGC 537
               |||||| |||||   |||  | || || ||||| || ||||||
Db         561 CATCGGTGACGCACACACCATCGGCACTCGTCCGGACAACGGC 603


RESULT 9
US-10-416-708A-9
; Sequence 9, Application US/10416708A
; Publication No. US20040161753A1
; GENERAL INFORMATION:
;  APPLICANT: Wise, John G.
;  APPLICANT:  Fromknecht, Katja
;  TITLE OF INVENTION: CREATION AND IDENTIFICATION OF PROTEINS HAVING NEW DNA BINDING
;  TITLE OF INVENTION:  SPECIFICITIES
;  FILE REFERENCE: 37779-0004
;  CURRENT APPLICATION NUMBER: US/10/416,708A
;  CURRENT FILING DATE:  2004-01-28
;  NUMBER OF SEQ ID NOS: 89
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
;   LENGTH: 3660
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Plasmid containing a promoter, cauliflower mosaic virus-derived
;   OTHER INFORMATION: target operator and reporter gene and ompA-derived separator gene
;   FEATURE:
```

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;   NAME/KEY: misc_binding
;   LOCATION: (1)..(28)
;   OTHER INFORMATION: cauliflower mosaic virus derived target DNA sequence
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (55)..(636)
;   OTHER INFORMATION: ompA separation tag fusion
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (64)..(608)
;   OTHER INFORMATION: E. coli ompA derived DNA sequence
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (608)..(684)
;   OTHER INFORMATION: separation tag DNA sequence
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (685)..(3660)
;   OTHER INFORMATION: pP2HIV1-derived DNA sequence
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (718)..(1164)
;   OTHER INFORMATION: lacZ' fragment
US-10-416-708A-9

  Query Match           28.9%;  Score 298.6;  DB 17;  Length 3660;
  Best Local Similarity   77.2%;  Pred. No. 1.9e-86;
  Matches  402;  Conservative    0;  Mismatches   89;  Indels   30;  Gaps    2;

Qy         15 CGTACTGAATGCGGCTCCGAAAGATAACACCTGGTATGCAGGTGGTAAACTGGGTTGGTC 74
Db        111 CGTAGCGCAGGCCGCTCCGAAAGATAACACCTGGTACACTGGTGCTAAACTGGGCTGGTC 170

Qy         75 CCAGTATCACGACACCGGTTTCTACGGTAACGGTTTCCAGAACAACAACGGTCCGACCCG 134
Db        171 CCAGTACCATGACACTGGTTTCATC--------------AACAACAATGGCCCGACCCA 215

Qy        135 TAACGATCAGCTTGGTGCTGGTGCGTTCGGTGGTTACCAGGTTAACCCGTACCTCGGTTT 194
Db        216 TGAAAACCAACTGGGCGCTGGTGCTTTTGGTGGTTACCAGGTTAACCCGTATGTTGGCTT 275

Qy        195 CGAAATGGGTTATGACTGGCTGGGCCGTATGGCATATAAAGGCAGCGTTGACAACGGTGC 254
Db        276 TGAAATGGGTTACGACTGGTTAGGTCGTATGCCGTACAAAGGCAGCGTTGAAAACGGTGC 335

Qy        255 TTTCAAAGCTCAGGGCGTTCAGCTGACCGCTAAACTGGGTTACCCGATCACTGACGATCT 314
Db        336 ATACAAAGCTCAGGGCGTTCAACTGACCGCTAAACTGGGTTACCCAATCACTGACGACCT 395

Qy        315 GGACATCTACACCCGTCTGGGCGGCATGGTTTGGCGCGCTGACTCCAAAGGCAACTACGC 374
Db        396 GGACATCTACACTCGTCTGGGTGGCATGGTATGGCGTGCAGACACTAAATCCAA------ 449

Qy        375 TTCTACCGGCGTTTCCCGTAGCGAACACGACACTGGCGTTTCCCCAGTATTTGCTGGCGG 434
Db        450 ---------CGTTTATGGTAAAAACCACGACACCGGCGTTTCTCCGGTCTTCGCTGGCGG 500

Qy        435 CGTAGAGTGGGCTGTTACTCGTGACATCGCTACCCGTCTGGAATACCAGTGGGTTAACAA 494
Db        501 TGTTGAGTACGCGATCACTCCTGAAATCGCTACCCGTCTGGAATACCAGTGGACCAACAA 560

Qy        495 CATCGGCGACGCGGGCACTGTGGGTACCCGTCCTGATAACG 535
Db        561 CATCGGTGACGCACACACCATCGGCACTCGTCCGGACAACG 601


RESULT 10
US-10-416-708A-62
; Sequence 62, Application US/10416708A
; Publication No. US20040161753A1
; GENERAL INFORMATION:
;  APPLICANT: Wise, John G.
;  APPLICANT:  Fromknecht, Katja
;  TITLE OF INVENTION: CREATION AND IDENTIFICATION OF PROTEINS HAVING NEW DNA BINDING
;  TITLE OF INVENTION:  SPECIFICITIES
;  FILE REFERENCE: 37779-0004
;  CURRENT APPLICATION NUMBER: US/10/416,708A
;  CURRENT FILING DATE:  2004-01-28
;  NUMBER OF SEQ ID NOS: 89
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 62
;   LENGTH: 4543
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Plasmid 2 for bacterial transcriptional activation screening
;   FEATURE:
;   NAME/KEY: misc_binding
;   LOCATION: (12)..(63)
;   OTHER INFORMATION: zif binding site and spacer
;   FEATURE:
;   NAME/KEY: promoter
;   LOCATION: (68)..(110)
;   OTHER INFORMATION: weak promoter
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (137)..(799)
;   OTHER INFORMATION: HIS3 fragment
;   FEATURE:
;   NAME/KEY: terminator
;   LOCATION: (800)..(847)
;   FEATURE:
;   NAME/KEY: misc_binding
;   LOCATION: (3068)..(3119)
;   OTHER INFORMATION: zif binding and spacer
;   FEATURE:
;   NAME/KEY: promoter
;   LOCATION: (3124)..(3166)
;   OTHER INFORMATION: weak promoter
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (3198)..(3782)
;   OTHER INFORMATION: ompA separation tag fusion
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (3861)..(4310)
;   OTHER INFORMATION: lacZ' fragment
US-10-416-708A-62

  Query Match           28.9%;  Score 298.6;  DB 17;  Length 4543;
  Best Local Similarity   77.2%;  Pred. No. 2.1e-86;
  Matches  402;  Conservative    0;  Mismatches   89;  Indels   30;  Gaps    2;

Qy         15 CGTACTGAATGCGGCTCCGAAAGATAACACCTGGTATGCAGGTGGTAAACTGGGTTGGTC 74
Db       3254 CGTAGCGCAGGCCGCTCCGAAAGATAACACCTGGTACACTGGTGCTAAACTGGGCTGGTC 3313

Qy         75 CCAGTATCACGACACCGGTTTCTACGGTAACGGTTTCCAGAACAACAACGGTCCGACCCG 134
Db       3314 CCAGTACCATGACACTGGTTTCATC--------------AACAACAATGGCCCGACCCA 3358

Qy        135 TAACGATCAGCTTGGTGCTGGTGCGTTCGGTGGTTACCAGGTTAACCCGTACCTCGGTTT 194
Db       3359 TGAAAACCAACTGGGCGCTGGTGCTTTTGGTGGTTACCAGGTTAACCCGTATGTTGGCTT 3418

Qy        195 CGAAATGGGTTATGACTGGCTGGGCCGTATGGCATATAAAGGCAGCGTTGACAACGGTGC 254
Db       3419 TGAAATGGGTTACGACTGGTTAGGTCGTATGCCGTACAAAGGCAGCGTTGAAAACGGTGC 3478

Qy        255 TTTCAAAGCTCAGGGCGTTCAGCTGACCGCTAAACTGGGTTACCCGATCACTGACGATCT 314
Db       3479 ATACAAAGCTCAGGGCGTTCAACTGACCGCTAAACTGGGTTACCCAATCACTGACGACCT 3538

Qy        315 GGACATCTACACCCGTCTGGGCGGCATGGTTTGGCGCGCTGACTCCAAAGGCAACTACGC 374
Db       3539 GGACATCTACACTCGTCTGGGTGGCATGGTATGGCGTGCAGACACTAAATCCAA------ 3592
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Qy        375 TTCTACCGGCGTTTCCCGTAGCGAACACGACACTGGCGTTTCCCCAGTATTTGCTGGCGG 434
              |||||   |||   | |||||||| |||||||| || || || ||||||||
Db       3593 ---------CGTTTATGGTAAAAACCACGACACCGGCGTTTCTCCGGTCTTCGCTGGCGG 3643

Qy        435 CGTAGAGTGGGCTGTTACTCGTGACATCGCTACCCGTCTGGAATACCAGTGGGTTAACAA 494
               || ||||  ||  | |||| ||| |||||||||||||||||||||||||   |||||
Db       3644 TGTTGAGTACGCGATCACTCCTGAAATCGCTACCCGTCTGGAATACCAGTGGACCAACAA 3703

Qy        495 CATCGGCGACGCGGGCACTGTGGGTACCCGTCCTGATAACG 535
              |||||| |||||   |||  | || || ||||| || ||||
Db       3704 CATCGGTGACGCACACACCATCGGCACTCGTCCGGACAACG 3744


RESULT 11
US-10-033-399B-24
; Sequence 24, Application US/10033399B
; Publication No. US20030104355A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, Caili
;  APPLICANT:  Zhong, Pingyu
;  APPLICANT:  Wang, Xinwei
;  TITLE OF INVENTION: ADAPTER-DIRECTED DISPLAY SYSTEMS
;  FILE REFERENCE: 13403.0005NPUS00
;  CURRENT APPLICATION NUMBER: US/10/033,399B
;  CURRENT FILING DATE:  2002-11-15
;  NUMBER OF SEQ ID NOS: 26
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
;   LENGTH: 3817
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic, comprising GABAB receptor 2, Lpp-OmpA gene sequence
US-10-033-399B-24

  Query Match             21.2%;  Score 219;  DB 15;  Length 3817;
  Best Local Similarity   76.3%;  Pred. No. 2.1e-60;
  Matches  289;  Conservative    0;  Mismatches   75;  Indels   15;  Gaps    1;

Qy        172 CAGGTTAACCCGTACCTCGGTTTCGAAATGGGTTATGACTGGCTGGGCCGTATGGCATAT 231
              | ||  |||||||| | || || |||||||||||| |||||| | || |||||| | ||
Db        262 CTGGGCAACCCGTATGTTGGCTTTGAAATGGGTTACGACTGGTTAGGTCGTATGCCGTAC 321

Qy        232 AAAGGCAGCGTTGACAACGGTGCTTTCAAAGCTCAGGGCGTTCAGCTGACCGCTAAACTG 291
              |||||||||||||| |||||||| | |||||||||||||||||| ||||||||||||||
Db        322 AAAGGCAGCGTTGAAAACGGTGCATACAAAGCTCAGGGCGTTCAACTGACCGCTAAACTG 381

Qy        292 GGTTACCCGATCACTGACGATCTGGACATCTACACCCGTCTGGGCGGCATGGTTTGGCGC 351
              |||||||| |||||||||| |||||||||||||| |||||||| |||||||| |||||
Db        382 GGTTACCCAATCACTGACGACCTGGACATCTACACTCGTCTGGGTGGCATGGTATGGCGT 441

Qy        352 GCTGACTCCAAAGGCAACTACGCTTCTACCGGCGTTTCCCGTAGCGAACACGACACTGGC 411
              || ||| | |||  |||                |||||   |||   | |||||||| |||
Db        442 GCAGACACTAAATCCAA---------------CGTTTATGGTAAAAACCACGACACCGGC 486

Qy        412 GTTTCCCCAGTATTTGCTGGCGGCGTAGAGTGGGCTGTTACTCGTGACATCGCTACCCGT 471
              |||||  || ||  || |||||||| || ||||   ||  | ||||  ||| ||||||||||||
Db        487 GTTTCTCCGGTCTTCGCTGGCGGTGTTGAGTACGCGATCACTCCTGAAATCGCTACCCGT 546

Qy        472 CTGGAATACCAGTGGGTTAACAACATCGGCGACGCGGGCACTGTGGGTACCCGTCCTGAT 531
              ||||||||||||||   |||||||||| |||||   |||  | ||  || |||||  ||
Db        547 CTGGAATACCAGTGGACGAACAACATCGGTGACGCACACACCATCGGCACTCGTCCGGAC 606

Qy        532 AACGGCATGCTGAGCCTGG 550
              || |     ||||||
Db        607 GGAGGTACATCCCGCCTGG 625


RESULT 12
US-09-809-665A-150
; Sequence 150, Application US/09809665A
; Publication No. US20040110268A1
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; GENERAL INFORMATION:
;  APPLICANT: Lowery E., David, et al.
;  TITLE OF INVENTION: Anti-Bacterial Vaccine Compositions
;  FILE REFERENCE: 28341/00435
;  CURRENT APPLICATION NUMBER: US/09/809,665A
;  CURRENT FILING DATE:  2001-03-15
;  PRIOR APPLICATION NUMBER: 60/153,453
;  PRIOR FILING DATE: 1999-09-10
;  PRIOR APPLICATION NUMBER: 60/128,689
;  PRIOR FILING DATE: 1999-04-09
;  PRIOR APPLICATION NUMBER: 09/545,199
;  PRIOR FILING DATE: 2000-04-06
;  NUMBER OF SEQ ID NOS: 197
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 150
;   LENGTH: 1095
;   TYPE: DNA
;   ORGANISM: Actinobacillus pleuropneumoniae
;   FEATURE:
;   OTHER INFORMATION: Omp5-2
;   NAME/KEY: CDS
;   LOCATION: (1)..(1092)
US-09-809-665A-150

  Query Match             15.6%;  Score 161;  DB 11;  Length 1095;
  Best Local Similarity   56.4%;  Pred. No. 1.2e-41;
  Matches  340;  Conservative    0;  Mismatches  260;  Indels    3;  Gaps    2;

Qy        414 TTCCCCAGTATTTGCTGGCGGCGTAGAGTGGGCTGTTACTCGTGACATCGCTACCCGTCT 473
              |||   | | || | ||  || || ||||  ||  ||  || |||  | ||  | ||| |
Db        483 TTCTTTAATTTTAGGTGCGGGTGTTGAGTACGCAATTCTTCCTGAATTAGCGGCACGTGT 542

Qy        474 GGAATACCAGTGGGTTAACAACATCGGCGACGCGGGCACTGTGGGTACCCGTCCTGATAA 533
              |||||||| ||| | ||||||   ||  | ||  ||         |     || |
Db        543 TGAATACCAATGGTTAAACAACGCAGGTAAAGCAAGCTACTCTACTTTAAATCGTATGGG 602

Qy        534 CGGCA-TGCTGAGCCTGGGCGTTTCCTACCGCTTCGGTCAGGAAGATGCTGC--ACCGGT 590
              | | ||   | | |  |  | ||    |  |      ||||   | ||| |      |
Db        603 TGCAACTGACTACCGTTCGGATATCAGTTCCGTATCTGCAGGTTTAAGCTACCGTTTCGG 662

Qy        591 TGTTGCTCCGGCTCCGGCTCCGGCTCCGGAAGTGGCTACCAAGCACTTCACCCTGAAGTC 650
              |   | | |||| |||| | | ||||||| ||| |  || ||  ||||| |  | |  ||
Db        663 TCAAGGTGCGGCACCGGTTGCAGCTCCGGCAGTTGAAACTAAAAACTTCGCATTCAGCTC 722

Qy        651 TGACGTTCTGTTCAACTTCAACAAAGCTACCCTGAAACCGGAAGGTCAGCAGGCTCTGGA 710
              ||||||  | |||   |||  ||| | | | | |||||||  |         ||  | ||
Db        723 TGACGTATTATTCGCATTCGGTAAATCAAACTTAAAACCGGCTGCGGCAACAGCATTAGA 782

Qy        711 TCAGCTGTACACTCAGCTGAGCAACATGGATCCGAAAGACGGTTCCGCTGTTGTTCTGGG 770
              |    || | ||  |  | |  |||  | |      | | | | |       ||    ||
Db        783 TGCAATGCAAACCGAAATCAATAACGCAGGTTTATCAAATGCTGCGATCCAAGTAAACGG 842

Qy        771 CTACACCGACCGCATCGGTTCCGAAGCTTACAACCAGCAGCTGTCTGAGAAACGTGCTCA 830
              |||||  |||||  |||||||   |||||||  |||    | ||  ||  |||||  |
Db        843 TTACACGGACCGTATCGGTAAAGAAGCTTCAAACTTAAAACTTTCACAACGTCGTGCGGA 902

Qy        831 GTCCGTTGTTGACTACCTGGTTGCTAAAGGCATCCCGGCTGGCAAAATCTCCGCTCGCGG 890
              | || | |||||  | ||| |||||||    |||||  |  ||  |  | ||    ||
Db        903 AACAGTAGCTAACTACATCGTTTCTAAAGGTGCTCCGGCAGCTAACGTAACTGCAGTAGG 962

Qy        891 CATGGGTGAATCCAACCCGGTTACTGGCAACACCTGTGACAACGTGAAAGCTCGCGCTGC 950
              ||||||  | ||||| || || |||   || |||||||| || |||| |||    ||
Db        963 TTACGGTGAAGCAAACCCTGTAACCGGCGCAACATGTGACAAAGTTAAAGGTCGTAAAGC 1022

Qy        951 CCTGATCGATTGCCTGGCTCCGGATCGTCGTGTAGAGATCGAAGTTAAAGGCTACAAAGA 1010
              | |||| |||| | || |||||||||||||| ||  |  |||||  ||||    |||||
Db       1023 ATTAATCGCTTGCTTAGCACCGGATCGTCGTGTTGAAGTTCAAGTTCAAGGTACTAAAGA 1082

Qy       1011 AGT 1013
              |||
Db       1083 AGT 1085
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RESULT 13
US-10-854-299-150
; Sequence 150, Application US/10854299
; Publication No. US20050003512A1
; GENERAL INFORMATION:
;  APPLICANT: Lowery E., David, et al.
;  TITLE OF INVENTION: Anti-Bacterial Vaccine Compositions
;  FILE REFERENCE: 28341/00435
;  CURRENT APPLICATION NUMBER: US/10/854,299
;  CURRENT FILING DATE:  2004-05-26
;  PRIOR APPLICATION NUMBER: 60/153,453
;  PRIOR FILING DATE: 1999-09-10
;  PRIOR APPLICATION NUMBER: 60/128,689
;  PRIOR FILING DATE: 1999-04-09
;  PRIOR APPLICATION NUMBER: 09/545,199
;  PRIOR FILING DATE: 2000-04-06
;  NUMBER OF SEQ ID NOS: 197
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 150
;   LENGTH: 1095
;   TYPE: DNA
;   ORGANISM: Actinobacillus pleuropneumoniae
;   FEATURE:
;   OTHER INFORMATION: Omp5-2
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1092)
US-10-854-299-150

  Query Match             15.6%;  Score 161;  DB 18;  Length 1095;
  Best Local Similarity   56.4%;  Pred. No. 1.2e-41;
  Matches  340;  Conservative    0;  Mismatches  260;  Indels    3;  Gaps    2;

Qy        414 TTCCCCAGTATTTGCTGGCGGCGTAGAGTGGGCTGTTACTCGTGACATCGCTACCCGTCT 473
              |||   | || | ||  || || ||||  ||  ||  || |||  | ||  | ||| |
Db        483 TTCTTTAATTTTAGGTGCGGGTGTTGAGTACGCAATTCTTCCTGAATTAGCGGCACGTGT 542

Qy        474 GGAATACCAGTGGGTTAACAACATCGGCGACGCGGGCACTGTGGGTACCCGTCCTGATAA 533
              |||||||| ||| | ||||||   ||  | ||  ||         |     || |
Db        543 TGAATACCAATGGTTAAACAACGCAGGTAAAGCAAGCTACTCTACTTTAAATCGTATGGG 602

Qy        534 CGGCA-TGCTGAGCCTGGGCGTTTCCTACCGCTTCGGTCAGGAAGATGCTGC--ACCGGT 590
              | | ||   | | |  | | ||   |  |     ||||   | ||| |     |
Db        603 TGCAACTGACTACCGTTCGGATATCAGTTCCGTATCTGCAGGTTTAAGCTACCGTTTCGG 662

Qy        591 TGTTGCTCCGGCTCCGGCTCCGGCTCCGGAAGTGGCTACCAAGCACTTCACCCTGAAGTC 650
              |   | | |||| |||| | | ||||||| ||| |  || ||  ||||| |  | |  ||
Db        663 TCAAGGTGCGGCACCGGTTGCAGCTCCGGCAGTTGAAACTAAAAACTTCGCATTCAGCTC 722

Qy        651 TGACGTTCTGTTCAACTTCAACAAAGCTACCCTGAAACCGGAAGGTCAGCAGGCTCTGGA 710
              ||||||  | |||   |||   ||| | | | | |||||||  |         ||  | ||
Db        723 TGACGTATTATTCGCATTCGGTAAATCAAACTTAAAACCGGCTGCGGCAACAGCATTAGA 782

Qy        711 TCAGCTGTACACTCAGCTGAGCAACATGGATCCGAAAGACGGTTCCGCTGTTGTTCTGGG 770
              |    || | ||  |  | |  |||   | |     | | | |        ||    ||
Db        783 TGCAATGCAAACCGAAATCAATAACGCAGGTTTATCAAATGCTGCGATCCAAGTAAACGG 842

Qy        771 CTACACCGACCGCATCGGTTCCGAAGCTTACAACCAGCAGCTGTCTGAGAAACGTGCTCA 830
              |||||  |||||  ||||||   |||||||  |||     | || ||  |     |||||  |
Db        843 TTACACGGACCGTATCGGTAAAGAAGCTTCAAACTTAAAACTTTCACAACGTCGTGCGGA 902

Qy        831 GTCCGTTGTTGACTACCTGGTTGCTAAAGGCATCCCGGCTGGCAAAATCTCCGCTCGCGG 890
              | || | | |||| | ||| |||||||     |||||  |  ||  |  | ||    ||
Db        903 AACAGTAGCTAACTACATCGTTTCTAAAGGTGCTCCGGCAGCTAACGTAACTGCAGTAGG 962

Qy        891 CATGGGTGAATCCAACCCGGTTACTGGCAACACCTGTGACAACGTGAAAGCTCGCGCTGC 950
              ||||||  | ||||| || || |||   || ||||||| || |||| |||    ||
Db        963 TTACGGTGAAGCAAACCCTGTAACCGGCGCAACATGTGACAAAGTTAAAGGTCGTAAAGC 1022

Qy        951 CCTGATCGATTGCCTGGCTCCGGATCGTCGTGTAGAGATCGAAGTTAAAGGCTACAAAGA 1010
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Db       1023 ATTAATCGCTTGCTTAGCACCGGATCGTCGTGTTGAAGTTCAAGTTCAAGGTACTAAAGA 1082

Qy        1011 AGT 1013
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Db        1083 AGT 1085


RESULT 14
US-10-770-824-7
; Sequence 7, Application US/10770824
; Publication No. US20040198954A1
; GENERAL INFORMATION:
;  APPLICANT: Campos, Manuel
;  APPLICANT:  Baarsch, Mary Jo
;  APPLICANT:  Rosey, Everett
;  APPLICANT:  Ankenbauer, Robert
;  APPLICANT:  Warren-Stewart, Lynn
;  APPLICANT:  Suiter, Brian
;  APPLICANT:  Keach, Robin
;  TITLE OF INVENTION: NOVEL PROTEINS FROM ACTINOBACILLUS PLEUROPNEUMONIAE
;  FILE REFERENCE: PC9854A
;  CURRENT APPLICATION NUMBER: US/10/770,824
;  CURRENT FILING DATE:  2004-02-03
;  PRIOR APPLICATION NUMBER: US/09/418,980
;  PRIOR FILING DATE: 1999-10-14
;  NUMBER OF SEQ ID NOS: 96
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
;   LENGTH: 1922
;   TYPE: DNA
;   ORGANISM: Actinobacillus pleuropneumoniae
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (614)..(1705)
US-10-770-824-7

  Query Match             15.4%;  Score 159.4;  DB 18;  Length 1922;
  Best Local Similarity   56.2%;  Pred. No. 5.1e-41;
  Matches  339;  Conservative    0;  Mismatches  261;  Indels    3;  Gaps    2;

Qy        414 TTCCCCAGTATTTGCTGGCGGCGTAGAGTGGGCTGTTACTCGTGACATCGCTACCCGTCT 473
              |||   | | || | ||  || || ||||  ||  ||  || |||  | ||  | ||| |
Db       1096 TTCTTTAATTTTAGGTGCGGGTGTTGAGTACGCAATTCTTCCTGAATTAGCGGCACGTGT 1155

Qy        474 GGAATACCAGTGGGTTAACAACATCGGCGACGCGGGCACTGTGGGTACCCGTCCTGATAA 533
              |||||||| ||| | ||||||   ||  | ||  ||         |     || |
Db       1156 TGAATACCAATGGTTAAACAACGCAGGTAAAGCAAGCTACTCTACTTTAAATCGTATGGG 1215

Qy        534 CGGCA-TGCTGAGCCTGGGCGTTTCCTACCGCTTCGGTCAGGAAGATGCTGC--ACCGGT 590
              | | ||   | | |  | | ||   |  |     ||||   | ||| |     |
Db       1216 TGCAACTGACTACCGTTCGGATATCAGTTCCGTATCTGCAGGTTTAAGCTACCGTTTCGG 1275

Qy        591 TGTTGCTCCGGCTCCGGCTCCGGCTCCGGAAGTGGCTACCAAGCACTTCACCCTGAAGTC 650
              |   | | |||  |||| | | ||||||| ||| |  || ||  |||| |  | |  ||
Db       1276 TCAAGGTGCGGTACCGGTTGCAGCTCCGGCAGTTGAAACTAAAAACTTCGCATTCAGCTC 1335

Qy        651 TGACGTTCTGTTCAACTTCAACAAAGCTACCCTGAAACCGGAAGGTCAGCAGGCTCTGGA 710
              ||||||  | |||   |||   ||| | | | | |||||||  |         ||  | ||
Db       1336 TGACGTATTATTCGCATTCGGTAAATCAAACTTAAAACCGGCTGCGGCAACAGCATTAGA 1395

Qy        711 TCAGCTGTACACTCAGCTGAGCAACATGGATCCGAAAGACGGTTCCGCTGTTGTTCTGGG 770
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Db       1396 TGCAATGCAAACCGAAATCAATAACGCAGGTTTATCAAATGCTGCGATCCAAGTAAACGG 1455

Qy        771 CTACACCGACCGCATCGGTTCCGAAGCTTACAACCAGCAGCTGTCTGAGAAACGTGCTCA 830
              |||||  |||||  ||||||   |||||||  |||     | || ||  |     |||||  |
Db       1456 TTACACGGACCGTATCGGTAAAGAAGCTTCAAACTTAAAACTTTCACAACGTCGTGCGGA 1515

Qy        831 GTCCGTTGTTGACTACCTGGTTGCTAAAGGCATCCCGGCTGGCAAAATCTCCGCTCGCGG 890
              | || | | |||| | ||| |||||||     |||||  |  ||  |  | ||    ||
Db       1516 AACAGTAGCTAACTACATCGTTTCTAAAGGTGCTCCGGCAGCTAACGTAACTGCAGTAGG 1575

Qy        891 CATGGGTGAATCCAACCCGGTTACTGGCAACACCTGTGACAACGTGAAAGCTCGCGCTGC 950
              ||||||  | ||||| || || |||   || ||||||| || |||| |||    ||
Db       1576 TTACGGTGAAGCAAACCCTGTAACCGGCGCAACATGTGACAAAGTTAAAGGTCGTAAAGC 1635
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Qy        951 CCTGATCGATTGCCTGGCTCCGGATCGTCGTGTAGAGATCGAAGTTAAAGGCTACAAAGA 1010
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Qy       1011 AGT 1013
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Db       1696 AGT 1698
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RESULT 15
US-10-336-840-20
; Sequence 20, Application US/10336840
; Publication No. US20030219454A1
; GENERAL INFORMATION:
; APPLICANT: TERRY, TAMSIN DEBORAH
; APPLICANT: TSENG, HSING-JU
; APPLICANT: HOBB, RHONDA IVY
; APPLICANT: JENNINGS, MICHAEL PAUL
; APPLICANT: DOWNES, JOHN
; TITLE OF INVENTION: HAEMAGGLUTININ ANTIGEN
; FILE REFERENCE: 37955-0007
; CURRENT APPLICATION NUMBER: US/10/336,840
; CURRENT FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: PCT/AU01/00822
; PRIOR FILING DATE: 2001-07-06
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 1035
; TYPE: DNA
; ORGANISM: Haemophilus paragallinarum
US-10-336-840-20

Query Match 13.0%; Score 135; DB 15; Length 1035;
Best Local Similarity 49.8%; Pred. No. 3.8e-33;
Matches 500; Conservative 0; Mismatches 475; Indels 30; Gaps 5;

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Qy         16 GTACTGAATGCGGCTCCGAAAGATAACACCTGGTATGCAGGTGGTAAACTGGGTTGGTCC 75
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Db         52 GTAGCACAAGCTGCACCACAAGCAAACACTTTCTATGCTGGTGCAAAAGCGGGCTGGGCA 111

Qy         76 CAGTATCACGACACCGGTTTCTACGGTAACGGTTTCCAGAACAACAACGGTCCGACCCGT 135
                 |||||          | |   | |    |  || ||      | ||| |    |||
Db        112 TCTTTCCACGATGGTTTAAACCAATTTGAAAACTCACAAAATGCAGATGGTACATTGCGT 171

Qy        136 AACGATCAGCTTGGTGCTGGTGCGTTCGGTGGTTACCAGGTTAACCCGTACCTCGGTTTC 195
              |   ||    |   |  ||| | ||||||||||||||  |||      || ||| | |
Db        172 A---ATTCTGTAACTTATGGGGTGTTCGGTGGTTACCAAATTACTGATAACTTCGCTGTT 228

Qy        196 GAAATGGGTTATGACTGGCTGGGCCGTATGGCATATAAAGGCAGCGTTGACAACGGTGCT 255
              ||  | ||||||||     | || |||      |           ||| ||| |  | |
Db        229 GAGCTAGGTTATGATGACTTTGGGCGTGCTAAACGCCGTCAAGGCGGTGAAACTGTTATA 288

Qy        256 ---TTCAAAGCTCAGGGCGTTCAGCTGACCGCTAAACTGGGTTACCCGATCACTGACGAT 312
                 | ||  | |||  || | |||  | | |   |||    |||| ||  |   ||| |
Db        289 AAATACACAAATCACGGAGCTCACTTAAGCTTAAAAGCAAGTTATCCAGTGCTTGAAGGA 348

Qy        313 CTGGACATCTACACCCGTCTGGGCGGCATGGTTTGGCGCGCTGACTCCAAAGGCAACTAC 372
              | ||  | ||  | ||  | || |    | |    ||  |||| |  |||   |   |
Db        349 TTAGATGTTTATGCTCGCGTTGGAGCAGCGTTGATTCGTTCTGATTATAAACCAACTAAA 408

Qy        373 GCTTCTACCGGCGTTTCCCGTAGCGAACACGACACTGGCGTTTCCCCAGTATTTGCTGGC 432
                 |  |       |         ||||||    |       ||||| |||||||| |||||
Db        409 AGAGCAGCTCCTAATCAGACGCACGAACATAGCTTAAAAGTTTCTCCAGTATTCGCTGGT 468

Qy        433 GGCGTAGAGTGGGCTGTTAC------TCGTGACATCGCTACCCGTCTGGAATACCAGTGG 486
              ||  ||||||      |  |       |  ||  | ||    ||| | ||||| || |||
Db        469 GGTTTAGAGTATAACTTACCATCATTACCAGAACTTGCATTACGTGTTGAATATCAATGG 528

Qy        487 GTTAACAACATCGGCGACGCGGGCACTGTGGGTACCCGTCCTGATAACGGCATGCTGAGC 546
              || || ||  | ||    | ||  |  |  |||| ||||   ||| |           | |
Db        529 GTAAATAAAGTAGGACGTGTGGAAAAAGATGGTAGCCGTGTAGATTATACACCAAGCATC 588
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Qy        547 CTGGGCGTTTCCTACCGCTTCGGTCAGGAAGATGCTGCACCGGTTGTTGCTCCGGCTCCG 606
                    ||  |     | ||                ||   |   ||| |      || ||
Db        589 GGTTCTGTAACTGCTGGTTTA-----------TCTTACCGTTTTGGTCAAAGTGCACCA 636

Qy        607 GCTCCGGCTCCGGAAGTGGCTACCAAGCACTTCACCCTGAAGTCTGACGTTCTGTTCAAC 666
              | |   |  ||  | || | | | ||    ||  |  | || || || |||   |||
Db        637 GTTGTTGAACCTAAGGTTGTTGCAAAAACATTTGCATTAAATTCAGATGTTACTTTCGCA 696

Qy        667 TTCAACAAAGCTACCCTGAAACCGGAAGGTCAGCAGGCTCTGGATCAGCTGTACACTCAG 726
              ||    ||||| |   |   || ||||  ||  | |   | ||     | ||    | |
Db        697 TTTGGTAAAGCAAATTTACGTCCAGAAGCACAAAATGTATTAGACGGTATTTATGGTGAA 756

Qy        727 CTGAGCAACATGGATCCGAAAGACGGTTCCGCTGTTGTTCTGGGCTACACCGACCGCATC 786
              |     |  | |  |   | | |           | ||||   || || || ||||| ||
Db        757 ATCGCACAGTTAAAATCAGTACAAGT------AGATGTTGCTGGTTATACTGACCGTATT 810

Qy        787 GGTTCCGAAGCTTACAACCAGCAGCTGTCTGAGAAACGTGCTCAGTCCGTTGTTGACTAC 846
              |||  ||||||   ||||  | |  | ||  |    |||||| |  | || | | |||||
Db        811 GGTAGCGAAGCAGCCAACTTGAAATTATCACAACGTCGTGCTGATACTGTGGCTAACTAC 870

Qy        847 CTGGTTGCTAAAGGCATCCCGGCTGGCAAAATCTCCGCTCGCGGCATGGGTGAATCCAAC 906
              | ||| |||||||  |  |     |    || ||  |    ||    |||||| | |||
Db        871 TTAGTTTCTAAAGGTGTTGCTCAAGAAGTGATTTCTTCAACAGGTTATGGTGAAGCGAAC 930

Qy        907 CCGGTTACTGGCAACACCTGTGACAACGTGAAAGCTCGCGCTGCCCTGATCGATTGCCTG 966
              || || |||||     |  ||||| |  || |||| ||||   ||  | |||| |||  |
Db        931 CCAGTAACTGGTGCGAAATGTGATACGGTTAAAGGTCGCAAAGCATTAATCGCTTGTTTA 990

Qy        967 GCTCCGGATCGTCGTGTAGAGATCGAAGTTAAAGGCTACAAAGAA 1011
              ||    |||||||||||||| |||  |||||||||  |   |  ||
Db        991 GCAGACGATCGTCGTGTAGAAATCTCAGTTAAAGGTGAAGAGTAA 1035
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Search completed: January 19, 2005, 18:13:24
Job time : 677 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: January 19, 2005, 13:35:28 ; Search time 116 Seconds
(without alignments)
6341.953 Million cell updates/sec

Title: US-09-913-772-1
Perfect score: 1035
Sequence: 1 atgaaagcaatttttcgtact.....taactcagccggcgggttaa 1035

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
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6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1009.8	97.6	1158	4	US-09-489-039A-280	Sequence 280, App
c 2	1009.8	97.6	1251	4	US-09-489-039A-367	Sequence 367, App
3	1008	97.4	1008	3	US-08-721-979A-13	Sequence 13, Appl
4	1008	97.4	1008	4	US-09-654-289-13	Sequence 13, Appl
5	1008	97.4	1008	4	US-09-582-876-13	Sequence 13, Appl
6	1008	97.4	1008	4	US-10-091-257-13	Sequence 13, Appl
7	1007	97.3	1007	3	US-08-836-500A-1	Sequence 1, Appli
8	1007	97.3	1007	4	US-09-679-750-1	Sequence 1, Appli
9	724.4	70.0	730	2	US-08-743-637B-11	Sequence 11, Appl
10	724.4	70.0	730	3	US-08-526-840B-11	Sequence 11, Appl
11	537	51.9	537	3	US-08-836-500A-3	Sequence 3, Appli
12	537	51.9	537	4	US-09-679-750-3	Sequence 3, Appli
13	460.4	44.5	1155	4	US-09-543-681A-3750	Sequence 3750, Ap
14	224.8	21.7	1273	1	US-07-794-731A-1	Sequence 1, Appli
15	224.8	21.7	1273	1	US-07-794-731A-2	Sequence 2, Appli
16	216	20.9	216	3	US-08-836-500A-5	Sequence 5, Appli
17	216	20.9	216	4	US-09-679-750-5	Sequence 5, Appli
18	161	15.6	1095	4	US-09-809-665A-150	Sequence 150, App
19	159.4	15.4	1922	4	US-09-418-980-7	Sequence 7, Appli
20	159	15.4	159	3	US-08-836-500A-7	Sequence 7, Appli
21	159	15.4	159	4	US-09-679-750-7	Sequence 7, Appli
22	133.2	12.9	1720	1	US-08-457-997B-1	Sequence 1, Appli
23	133.2	12.9	1720	3	US-08-467-722A-1	Sequence 1, Appli
24	133.2	12.9	1720	4	US-09-451-184-1	Sequence 1, Appli
25	130	12.6	1830121	4	US-09-557-884-1	Sequence 1, Appli
26	130	12.6	1830121	4	US-09-643-990A-1	Sequence 1, Appli
27	130	12.6	1830121	4	US-10-329-960-1	Sequence 1, Appli
28	129.8	12.5	1319	4	US-09-418-980-9	Sequence 9, Appli
29	127.2	12.3	1059	3	US-08-476-102A-3	Sequence 3, Appli
30	125	12.1	1110	4	US-09-809-665A-152	Sequence 152, App
31	110	10.6	184	1	US-08-375-241-12	Sequence 12, Appl
32	110	10.6	184	5	PCT-US92-06617A-12	Sequence 12, Appl
33	92.4	8.9	169	1	US-08-375-241-13	Sequence 13, Appl
34	92.4	8.9	169	5	PCT-US92-06617A-13	Sequence 13, Appl
c 35	69.4	6.7	640681	4	US-09-790-988-1	Sequence 1, Appli
36	57.6	5.6	708	4	US-09-252-991A-3024	Sequence 3024, Ap
c 37	57.6	5.6	711	4	US-09-252-991A-2929	Sequence 2929, Ap
38	56.6	5.5	486	2	US-08-572-447C-10	Sequence 10, Appl
39	56.6	5.5	486	3	US-09-267-747-10	Sequence 10, Appl
40	56.6	5.5	645	2	US-08-572-447C-12	Sequence 12, Appl
41	56.6	5.5	645	3	US-09-267-747-12	Sequence 12, Appl
42	56.6	5.5	681	2	US-08-572-447C-14	Sequence 14, Appl
43	56.6	5.5	681	3	US-09-267-747-14	Sequence 14, Appl
44	56	5.4	534	4	US-09-252-991A-12949	Sequence 12949, A
45	56	5.4	819	4	US-09-252-991A-13110	Sequence 13110, A

ALIGNMENTS

RESULT 1
US-09-489-039A-280
; Sequence 280, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 280
; LENGTH: 1158
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-280

Query Match 97.6%; Score 1009.8; DB 4; Length 1158;
Best Local Similarity 99.3%; Pred. No. 5.7e-277;
Matches 1014; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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Qy         15 CGTACTGAATGCGGCTCCGAAAGATAACACCTGGTATGCAGGTGGTAAACTGGGTTGGTC 74
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Db        138 CGTAGCGCAGGCCGCTCCGAAAGATAACACCTGGTATGCAGGTGGTAAACTGGGTTGGTC 197

Qy         75 CCAGTATCACGACACCGGTTTCTACGGTAACGGTTTCCAGAACAACAACGGTCCGACCCG 134
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        198 CCAGTATCACGACACCGGTTTCTACGGTAACGGTTTCCAGAACAACAACGGTCCGACCCG 257

Qy        135 TAACGATCAGCTTGGTGCTGGTGCGTTCGGTGGTTACCAGGTTAACCCGTACCTCGGTTT 194
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        258 TAACGATCAGCTTGGTGCTGGTGCGTTCGGTGGTTACCAGGTTAACCCGTACCTCGGTTT 317

Qy        195 CGAAATGGGTTATGACTGGCTGGGCCGTATGGCATATAAAGGCAGCGTTGACAACGGTGC 254
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        318 CGAAATGGGTTATGACTGGCTGGGCCGTATGGCATATAAAGGCAGCGTTGACAACGGTGC 377

Qy        255 TTTCAAAGCTCAGGGCGTTCAGCTGACCGCTAAACTGGGTTACCCGATCACTGACGATCT 314
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        378 TTTCAAAGCTCAGGGCGTTCAGCTGACCGCTAAACTGGGTTACCCGATCACTGACGATCT 437

Qy        315 GGACATCTACACCCGTCTGGGCGGCATGGTTTGGCGCGCTGACTCCAAAGGCAACTACGC 374
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        438 GGACATCTACACCCGTCTGGGCGGCATGGTTTGGCGCGCTGACTCCAAAGGCAACTACGC 497

Qy        375 TTCTACCGGCGTTTCCCGTAGCGAACACGACACTGGCGTTTCCCCAGTATTTGCTGGCGG 434
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Db        498 TTCTACCGGCGTTTCCCGTAGCGAACACGACACTGGCGTTTCCCCAGTATTTGCTGGCGG 557

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Db        558 CGTAGAGTGGGCTGTTACTCGTGACATCGCTACCCGTCTGGAATACCAGTGGGTTAACAA 617

Qy        495 CATCGGCGACGCGGGCACTGTGGGTACCCGTCCTGATAACGGCATGCTGAGCCTGGGCGT 554
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Db        618 CATCGGCGACGCGGGCACCGTGGGTACCCGTCCTGATAACGGCATGCTGAGCCTGGGCGT 677

Qy        555 TTCCTACCGCTTCGGTCAGGAAGATGCTGCACCGGTTGTTGCTCCGGCTCCGGCTCCGGC 614
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Db        678 TTCCTACCGCTTCGGTCAGGAAGATGCTGCACCGGTTGTTGCTCCGGCTCCGGCTCCGGC 737

Qy        615 TCCGGAAGTGGCTACCAAGCACTTCACCCTGAAGTCTGACGTTCTGTTCAACTTCAACAA 674
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        738 TCCGGAAGTGGCTACCAAGCACTTCACCCTGAAGTCTGACGTTCTGTTCAACTTCAACAA 797

Qy        675 AGCTACCCTGAAACCGGAAGGTCAGCAGGCTCTGGATCAGCTGTACACTCAGCTGAGCAA 734
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Db        798 AGCTACCCTGAAACCGGAAGGTCAGCAGGCTCTGGATCAGCTGTACACTCAGCTGAGCAA 857

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Db        858 CATGGATCCGAAAGACGGTTCCGCTGTTGTTCTGGGCTACACCGACCGCATCGGTTCCGA 917

Qy        795 AGCTTACAACCAGCAGCTGTCTGAGAAACGTGCTCAGTCCGTTGTTGACTACCTGGTTGC 854
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Db        918 AGCTTACAACCAGCAGCTGTCTGAGAAACGTGCTCAGTCCGTTGTTGACTACCTGGTTGC 977

Qy        855 TAAAGGCATCCCGGCTGGCAAAATCTCCGCTCGCGGCATGGGTGAATCCAACCCGGTTAC 914
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Qy        915 TGGCAACACCTGTGACAACGTGAAAGCTCGCGCTGCCCTGATCGATTGCCTGGCTCCGGA 974
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Qy        975 TCGTCGTGTAGAGATCGAAGTTAAAGGCTACAAAGAAGTTGTAACTCAGCCGGCGGGTTA 1034
              |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db       1098 TCGTCGTGTAGAGATCGAAGTTAAAGGCTACAAAGAAGTTGTAACTCAGCCGGCGGCTTA 1157

Qy       1035 A 1035
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Db       1158 A 1158


RESULT 2
US-09-489-039A-367/c
; Sequence 367, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
;  APPLICANT:  Gary Breton et. al
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
;  TITLE OF INVENTION:  PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  2709.2004001
;  CURRENT APPLICATION NUMBER: US/09/489,039A
;  CURRENT FILING DATE:  2000-01-27
;  PRIOR APPLICATION NUMBER:  US 60/117,747
;  PRIOR FILING DATE:  1999-01-29
;  NUMBER OF SEQ ID NOS:  14342
; SEQ ID NO 367
;   LENGTH: 1251
;   TYPE: DNA
;   ORGANISM: Klebsiella pneumoniae
US-09-489-039A-367

  Query Match            97.6%;  Score 1009.8;  DB 4;  Length 1251;
  Best Local Similarity  99.3%;  Pred. No. 5.9e-277;
  Matches 1014;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy         15 CGTACTGAATGCGGCTCCGAAAGATAACACCTGGTATGCAGGTGGTAAACTGGGTTGGTC 74
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Db       1165 CGTAGCGCAGGCCGCTCCGAAAGATAACACCTGGTATGCAGGTGGTAAACTGGGTTGGTC 1106

Qy         75 CCAGTATCACGACACCGGTTTCTACGGTAACGGTTTCCAGAACAACAACGGTCCGACCCG 134
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1105 CCAGTATCACGACACCGGTTTCTACGGTAACGGTTTCCAGAACAACAACGGTCCGACCCG 1046

Qy        135 TAACGATCAGCTTGGTGCTGGTGCGTTCGGTGGTTACCAGGTTAACCCGTACCTCGGTTT 194
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1045 TAACGATCAGCTTGGTGCTGGTGCGTTCGGTGGTTACCAGGTTAACCCGTACCTCGGTTT 986

Qy        195 CGAAATGGGTTATGACTGGCTGGGCCGTATGGCATATAAAGGCAGCGTTGACAACGGTGC 254
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        985 CGAAATGGGTTATGACTGGCTGGGCCGTATGGCATATAAAGGCAGCGTTGACAACGGTGC 926

Qy        255 TTTCAAAGCTCAGGGCGTTCAGCTGACCGCTAAACTGGGTTACCCGATCACTGACGATCT 314
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        925 TTTCAAAGCTCAGGGCGTTCAGCTGACCGCTAAACTGGGTTACCCGATCACTGACGATCT 866

Qy        315 GGACATCTACACCCGTCTGGGCGGCATGGTTTGGCGCGCTGACTCCAAAGGCAACTACGC 374
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        865 GGACATCTACACCCGTCTGGGCGGCATGGTTTGGCGCGCTGACTCCAAAGGCAACTACGC 806

Qy        375 TTCTACCGGCGTTTCCCGTAGCGAACACGACACTGGCGTTTCCCCAGTATTTGCTGGCGG 434
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        805 TTCTACCGGCGTTTCCCGTAGCGAACACGACACTGGCGTTTCCCCAGTATTTGCTGGCGG 746

Qy        435 CGTAGAGTGGGCTGTTACTCGTGACATCGCTACCCGTCTGGAATACCAGTGGGTTAACAA 494
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        745 CGTAGAGTGGGCTGTTACTCGTGACATCGCTACCCGTCTGGAATACCAGTGGGTTAACAA 686

Qy        495 CATCGGCGACGCGGGCACTGTGGGTACCCGTCCTGATAACGGCATGCTGAGCCTGGGCGT 554
              |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db        685 CATCGGCGACGCGGGCACCGTGGGTACCCGTCCTGATAACGGCATGCTGAGCCTGGGCGT 626

Qy        555 TTCCTACCGCTTCGGTCAGGAAGATGCTGCACCGGTTGTTGCTCCGGCTCCGGCTCCGGC 614
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        625 TTCCTACCGCTTCGGTCAGGAAGATGCTGCACCGGTTGTTGCTCCGGCTCCGGCTCCGGC 566

Qy        615 TCCGGAAGTGGCTACCAAGCACTTCACCCTGAAGTCTGACGTTCTGTTCAACTTCAACAA 674
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        565 TCCGGAAGTGGCTACCAAGCACTTCACCCTGAAGTCTGACGTTCTGTTCAACTTCAACAA 506

Qy        675 AGCTACCCTGAAACCGGAAGGTCAGCAGGCTCTGGATCAGCTGTACACTCAGCTGAGCAA 734
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Db        505 AGCTACCCTGAAACCGGAAGGTCAGCAGGCTCTGGATCAGCTGTACACTCAGCTGAGCAA 446

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Db        445 CATGGATCCGAAAGACGGTTCCGCTGTTGTTCTGGGCTACACCGACCGCATCGGTTCCGA 386

Qy        795 AGCTTACAACCAGCAGCTGTCTGAGAAACGTGCTCAGTCCGTTGTTGACTACCTGGTTGC 854
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Db        385 AGCTTACAACCAGCAGCTGTCTGAGAAACGTGCTCAGTCCGTTGTTGACTACCTGGTTGC 326

Qy        855 TAAAGGCATCCCGGCTGGCAAAATCTCCGCTCGCGGCATGGGTGAATCCAACCCGGTTAC 914
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        325 TAAAGGCATCCCGGCTGGCAAAATCTCCGCTCGCGGCATGGGTGAATCCAACCCGGTTAC 266

Qy        915 TGGCAACACCTGTGACAACGTGAAAGCTCGCGCTGCCCTGATCGATTGCCTGGCTCCGGA 974
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Db        265 TGGCAACACCTGTGACAACGTGAAAGCTCGCGCTGCCCTGATCGATTGCCTGGCTCCGGA 206

Qy        975 TCGTCGTGTAGAGATCGAAGTTAAAGGCTACAAAGAAGTTGTAACTCAGCCGGCGGGTTA 1034
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Db        205 TCGTCGTGTAGAGATCGAAGTTAAAGGCTACAAAGAAGTTGTAACTCAGCCGGCGGCTTA 146

Qy       1035 A 1035
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Db        145 A 145


RESULT 3
US-08-721-979A-13
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; Sequence 13, Application US/08721979A
; Patent No. 6113911
;  GENERAL INFORMATION:
;    APPLICANT:  Binz, Hans
;    APPLICANT:  N'Guyen, Ngoc Thien
;    APPLICANT:  Baussant, Thierry
;    APPLICANT:  Trudel, Michel
;    TITLE OF INVENTION:  PEPTIDE FRAGMENT OF RESPIRATORY
;    TITLE OF INVENTION:  SYNCYTIAL VIRUS PROTEIN G, IMMUNOGENIC AGENT,PHARMACEUTICAL
;    TITLE OF INVENTION:  COMPOSITION CONTAINING IT AND PREPARATION PROCESS
;    NUMBER OF SEQUENCES:  75
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Gordon W. Hueschen
;      STREET:  715 The "H" Bldg., 310 East Michigan
;      STREET:  Avenue
;      CITY:  Kalamazoo
;      STATE:  MI
;      COUNTRY:  USA
;      ZIP:  49007
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;      SOFTWARE:
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/721,979A
;      FILING DATE:  October 4, 1996
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  FR 94 04009
;      FILING DATE:  06-APR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hueschen, Gordon W.
;      REGISTRATION NUMBER:  16,157
;      REFERENCE/DOCKET NUMBER:  PF57PCTUS/dln
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  616-382-0030
;      TELEFAX:  616-382-2030
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1008 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..1008
;      OTHER INFORMATION:  /note= "name : P40"
US-08-721-979A-13

  Query Match             97.4%;  Score 1008;  DB 3;  Length 1008;
  Best Local Similarity   100.0%;  Pred. No. 1.8e-276;
  Matches 1008;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         28 GCTCCGAAAGATAACACCTGGTATGCAGGTGGTAAACTGGGTTGGTCCCAGTATCACGAC 87
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Db          1 GCTCCGAAAGATAACACCTGGTATGCAGGTGGTAAACTGGGTTGGTCCCAGTATCACGAC 60

Qy         88 ACCGGTTTCTACGGTAACGGTTTCCAGAACAACAACGGTCCGACCCGTAACGATCAGCTT 147
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ACCGGTTTCTACGGTAACGGTTTCCAGAACAACAACGGTCCGACCCGTAACGATCAGCTT 120

Qy        148 GGTGCTGGTGCGTTCGGTGGTTACCAGGTTAACCCGTACCTCGGTTTCGAAATGGGTTAT 207
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGTGCTGGTGCGTTCGGTGGTTACCAGGTTAACCCGTACCTCGGTTTCGAAATGGGTTAT 180

Qy        208 GACTGGCTGGGCCGTATGGCATATAAAGGCAGCGTTGACAACGGTGCTTTCAAAGCTCAG 267
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GACTGGCTGGGCCGTATGGCATATAAAGGCAGCGTTGACAACGGTGCTTTCAAAGCTCAG 240

Qy        268 GGCGTTCAGCTGACCGCTAAACTGGGTTACCCGATCACTGACGATCTGGACATCTACACC 327
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GGCGTTCAGCTGACCGCTAAACTGGGTTACCCGATCACTGACGATCTGGACATCTACACC 300

Qy        328 CGTCTGGGCGGCATGGTTTGGCGCGCTGACTCCAAAGGCAACTACGCTTCTACCGGCGTT 387
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Db        301 CGTCTGGGCGGCATGGTTTGGCGCGCTGACTCCAAAGGCAACTACGCTTCTACCGGCGTT 360

Qy        388 TCCCGTAGCGAACACGACACTGGCGTTTCCCCAGTATTTGCTGGCGGCGTAGAGTGGGCT 447
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TCCCGTAGCGAACACGACACTGGCGTTTCCCCAGTATTTGCTGGCGGCGTAGAGTGGGCT 420

Qy        448 GTTACTCGTGACATCGCTACCCGTCTGGAATACCAGTGGGTTAACAACATCGGCGACGCG 507
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GTTACTCGTGACATCGCTACCCGTCTGGAATACCAGTGGGTTAACAACATCGGCGACGCG 480

Qy        508 GGCACTGTGGGTACCCGTCCTGATAACGGCATGCTGAGCCTGGGCGTTTCCTACCGCTTC 567
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCACTGTGGGTACCCGTCCTGATAACGGCATGCTGAGCCTGGGCGTTTCCTACCGCTTC 540

Qy        568 GGTCAGGAAGATGCTGCACCGGTTGTTGCTCCGGCTCCGGCTCCGGCTCCGGAAGTGGCT 627
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GGTCAGGAAGATGCTGCACCGGTTGTTGCTCCGGCTCCGGCTCCGGCTCCGGAAGTGGCT 600

Qy        628 ACCAAGCACTTCACCCTGAAGTCTGACGTTCTGTTCAACTTCAACAAAGCTACCCTGAAA 687
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 ACCAAGCACTTCACCCTGAAGTCTGACGTTCTGTTCAACTTCAACAAAGCTACCCTGAAA 660

Qy        688 CCGGAAGGTCAGCAGGCTCTGGATCAGCTGTACACTCAGCTGAGCAACATGGATCCGAAA 747
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Db        661 CCGGAAGGTCAGCAGGCTCTGGATCAGCTGTACACTCAGCTGAGCAACATGGATCCGAAA 720

Qy        748 GACGGTTCCGCTGTTGTTCTGGGCTACACCGACCGCATCGGTTCCGAAGCTTACAACCAG 807
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Db        721 GACGGTTCCGCTGTTGTTCTGGGCTACACCGACCGCATCGGTTCCGAAGCTTACAACCAG 780

Qy        808 CAGCTGTCTGAGAAACGTGCTCAGTCCGTTGTTGACTACCTGGTTGCTAAAGGCATCCCG 867
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CAGCTGTCTGAGAAACGTGCTCAGTCCGTTGTTGACTACCTGGTTGCTAAAGGCATCCCG 840

Qy        868 GCTGGCAAAATCTCCGCTCGCGGCATGGGTGAATCCAACCCGGTTACTGGCAACACCTGT 927
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GCTGGCAAAATCTCCGCTCGCGGCATGGGTGAATCCAACCCGGTTACTGGCAACACCTGT 900

Qy        928 GACAACGTGAAAGCTCGCGCTGCCCTGATCGATTGCCTGGCTCCGGATCGTCGTGTAGAG 987
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GACAACGTGAAAGCTCGCGCTGCCCTGATCGATTGCCTGGCTCCGGATCGTCGTGTAGAG 960

Qy        988 ATCGAAGTTAAAGGCTACAAAGAAGTTGTAACTCAGCCGGCGGGTTAA 1035
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 ATCGAAGTTAAAGGCTACAAAGAAGTTGTAACTCAGCCGGCGGGTTAA 1008


RESULT 4
US-09-654-289-13
; Sequence 13, Application US/09654289
; Patent No. 6410030
;  GENERAL INFORMATION:
;    APPLICANT:  Binz, Hans
;    APPLICANT:  N'Guyen, Ngoc Thien
;    APPLICANT:  Baussant, Thierry
;    APPLICANT:  Trudel, Michel
;    TITLE OF INVENTION:  PEPTIDE FRAGMENT OF RESPIRATORY
;    TITLE OF INVENTION:  SYNCYTIAL VIRUS PROTEIN G, IMMUNOGENIC AGENT,PHARMACEUTICAL
;    TITLE OF INVENTION:  COMPOSITION CONTAINING IT AND PREPARATION PROCESS
;    NUMBER OF SEQUENCES:  75
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Gordon W. Hueschen
;      STREET:  715 The "H" Bldg., 310 East Michigan
;      STREET:  Avenue
;      CITY:  Kalamazoo
;      STATE:  MI
;      COUNTRY:  USA
;      ZIP:  49007
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;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;       SOFTWARE:
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/09/654,289
;       FILING DATE:
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/721,979
;       FILING DATE:
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Hueschen, Gordon W.
;       REGISTRATION NUMBER:  16,157
;       REFERENCE/DOCKET NUMBER:  PF57PCTUS/dln
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  616-382-0030
;       TELEFAX:  616-382-2030
;   INFORMATION FOR SEQ ID NO:  13:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  1008 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  1..1008
;       OTHER INFORMATION:  /note= "name : P40"
US-09-654-289-13

  Query Match             97.4%;  Score 1008;  DB 4;  Length 1008;
  Best Local Similarity   100.0%;  Pred. No. 1.8e-276;
  Matches 1008;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         28 GCTCCGAAAGATAACACCTGGTATGCAGGTGGTAAACTGGGTTGGTCCCAGTATCACGAC 87
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Db          1 GCTCCGAAAGATAACACCTGGTATGCAGGTGGTAAACTGGGTTGGTCCCAGTATCACGAC 60

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Db         61 ACCGGTTTCTACGGTAACGGTTTCCAGAACAACAACGGTCCGACCCGTAACGATCAGCTT 120

Qy        148 GGTGCTGGTGCGTTCGGTGGTTACCAGGTTAACCCGTACCTCGGTTTCGAAATGGGTTAT 207
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Qy        208 GACTGGCTGGGCCGTATGGCATATAAAGGCAGCGTTGACAACGGTGCTTTCAAAGCTCAG 267
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Db        421 GTTACTCGTGACATCGCTACCCGTCTGGAATACCAGTGGGTTAACAACATCGGCGACGCG 480

Qy        508 GGCACTGTGGGTACCCGTCCTGATAACGGCATGCTGAGCCTGGGCGTTTCCTACCGCTTC 567
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Db        481 GGCACTGTGGGTACCCGTCCTGATAACGGCATGCTGAGCCTGGGCGTTTCCTACCGCTTC 540

Qy        568 GGTCAGGAAGATGCTGCACCGGTTGTTGCTCCGGCTCCGGCTCCGGCTCCGGAAGTGGCT 627
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Db        541 GGTCAGGAAGATGCTGCACCGGTTGTTGCTCCGGCTCCGGCTCCGGCTCCGGAAGTGGCT 600

Qy        628 ACCAAGCACTTCACCCTGAAGTCTGACGTTCTGTTCAACTTCAACAAAGCTACCCTGAAA 687
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 ACCAAGCACTTCACCCTGAAGTCTGACGTTCTGTTCAACTTCAACAAAGCTACCCTGAAA 660

Qy        688 CCGGAAGGTCAGCAGGCTCTGGATCAGCTGTACACTCAGCTGAGCAACATGGATCCGAAA 747
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Db        661 CCGGAAGGTCAGCAGGCTCTGGATCAGCTGTACACTCAGCTGAGCAACATGGATCCGAAA 720

Qy        748 GACGGTTCCGCTGTTGTTCTGGGCTACACCGACCGCATCGGTTCCGAAGCTTACAACCAG 807
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Db        721 GACGGTTCCGCTGTTGTTCTGGGCTACACCGACCGCATCGGTTCCGAAGCTTACAACCAG 780

Qy        808 CAGCTGTCTGAGAAACGTGCTCAGTCCGTTGTTGACTACCTGGTTGCTAAAGGCATCCCG 867
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CAGCTGTCTGAGAAACGTGCTCAGTCCGTTGTTGACTACCTGGTTGCTAAAGGCATCCCG 840

Qy        868 GCTGGCAAAATCTCCGCTCGCGGCATGGGTGAATCCAACCCGGTTACTGGCAACACCTGT 927
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Db        841 GCTGGCAAAATCTCCGCTCGCGGCATGGGTGAATCCAACCCGGTTACTGGCAACACCTGT 900

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Db        961 ATCGAAGTTAAAGGCTACAAAGAAGTTGTAACTCAGCCGGCGGGTTAA 1008


RESULT 5
US-09-582-876-13
; Sequence 13, Application US/09582876
; Patent No. 6537556
;   GENERAL INFORMATION:
;       APPLICANT: Binz, Hans
;                  N'Guyen, Ngoc Thien
;                  Baussant, Thierry
;                  Trudel, Michel
;       TITLE OF INVENTION: PEPTIDE FRAGMENT OF RESPIRATORY
;                           SYNCYTIAL VIRUS PROTEIN G, IMMUNOGENIC AGENT,PHARMACEUTICAL
;                           COMPOSITION CONTAINING IT AND PREPARATION PROCESS
;       NUMBER OF SEQUENCES: 75
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Gordon W. Hueschen
;            STREET: 715 The "H" Bldg., 310 East Michigan
;                    Avenue
;            CITY: Kalamazoo
;            STATE: MI
;            COUNTRY: USA
;            ZIP: 49007
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;                      (EPO)
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/582,876
;            FILING DATE: 30-Jun-2000
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 08/721,979
;            FILING DATE: <Unknown>
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Hueschen, Gordon W.
;            REGISTRATION NUMBER: 16,157
;            REFERENCE/DOCKET NUMBER: PF57PCTUS/dln
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 616-382-0030
```

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;            TELEFAX: 616-382-2030
;   INFORMATION FOR SEQ ID NO: 13:
;        SEQUENCE CHARACTERISTICS:
;            LENGTH: 1008 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;        MOLECULE TYPE: peptide
;        FEATURE:
;            NAME/KEY:  CDS
;            LOCATION: 1..1008
;            OTHER INFORMATION: /note= "name : P40"
;        SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-582-876-13

  Query Match             97.4%;  Score 1008;  DB 4;  Length 1008;
  Best Local Similarity   100.0%;  Pred. No. 1.8e-276;
  Matches 1008;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         28 GCTCCGAAAGATAACACCTGGTATGCAGGTGGTAAACTGGGTTGGTCCCAGTATCACGAC 87
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Db          1 GCTCCGAAAGATAACACCTGGTATGCAGGTGGTAAACTGGGTTGGTCCCAGTATCACGAC 60

Qy         88 ACCGGTTTCTACGGTAACGGTTTCCAGAACAACAACGGTCCGACCCGTAACGATCAGCTT 147
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Db         61 ACCGGTTTCTACGGTAACGGTTTCCAGAACAACAACGGTCCGACCCGTAACGATCAGCTT 120

Qy        148 GGTGCTGGTGCGTTCGGTGGTTACCAGGTTAACCCGTACCTCGGTTTCGAAATGGGTTAT 207
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGTGCTGGTGCGTTCGGTGGTTACCAGGTTAACCCGTACCTCGGTTTCGAAATGGGTTAT 180

Qy        208 GACTGGCTGGGCCGTATGGCATATAAAGGCAGCGTTGACAACGGTGCTTTCAAAGCTCAG 267
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Db        181 GACTGGCTGGGCCGTATGGCATATAAAGGCAGCGTTGACAACGGTGCTTTCAAAGCTCAG 240

Qy        268 GGCGTTCAGCTGACCGCTAAACTGGGTTACCCGATCACTGACGATCTGGACATCTACACC 327
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Db        241 GGCGTTCAGCTGACCGCTAAACTGGGTTACCCGATCACTGACGATCTGGACATCTACACC 300

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Db        301 CGTCTGGGCGGCATGGTTTGGCGCGCTGACTCCAAAGGCAACTACGCTTCTACCGGCGTT 360

Qy        388 TCCCGTAGCGAACACGACACTGGCGTTTCCCCAGTATTTGCTGGCGGCGTAGAGTGGGCT 447
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Qy        448 GTTACTCGTGACATCGCTACCCGTCTGGAATACCAGTGGGTTAACAACATCGGCGACGCG 507
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Db        421 GTTACTCGTGACATCGCTACCCGTCTGGAATACCAGTGGGTTAACAACATCGGCGACGCG 480

Qy        508 GGCACTGTGGGTACCCGTCCTGATAACGGCATGCTGAGCCTGGGCGTTTCCTACCGCTTC 567
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Db        481 GGCACTGTGGGTACCCGTCCTGATAACGGCATGCTGAGCCTGGGCGTTTCCTACCGCTTC 540

Qy        568 GGTCAGGAAGATGCTGCACCGGTTGTTGCTCCGGCTCCGGCTCCGGCTCCGGAAGTGGCT 627
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Db        541 GGTCAGGAAGATGCTGCACCGGTTGTTGCTCCGGCTCCGGCTCCGGCTCCGGAAGTGGCT 600

Qy        628 ACCAAGCACTTCACCCTGAAGTCTGACGTTCTGTTCAACTTCAACAAAGCTACCCTGAAA 687
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Db        601 ACCAAGCACTTCACCCTGAAGTCTGACGTTCTGTTCAACTTCAACAAAGCTACCCTGAAA 660

Qy        688 CCGGAAGGTCAGCAGGCTCTGGATCAGCTGTACACTCAGCTGAGCAACATGGATCCGAAA 747
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Db        721 GACGGTTCCGCTGTTGTTCTGGGCTACACCGACCGCATCGGTTCCGAAGCTTACAACCAG 780

Qy        808 CAGCTGTCTGAGAAACGTGCTCAGTCCGTTGTTGACTACCTGGTTGCTAAAGGCATCCCG 867
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CAGCTGTCTGAGAAACGTGCTCAGTCCGTTGTTGACTACCTGGTTGCTAAAGGCATCCCG 840

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Db        841 GCTGGCAAAATCTCCGCTCGCGGCATGGGTGAATCCAACCCGGTTACTGGCAACACCTGT 900

Qy        928 GACAACGTGAAAGCTCGCGCTGCCCTGATCGATTGCCTGGCTCCGGATCGTCGTGTAGAG 987
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Db        961 ATCGAAGTTAAAGGCTACAAAGAAGTTGTAACTCAGCCGGCGGGTTAA 1008


RESULT 6
US-10-091-257-13
; Sequence 13, Application US/10091257
; Patent No. 6616930
;   GENERAL INFORMATION:
;        APPLICANT: Binz, Hans
;                   N'Guyen, Ngoc Thien
;                   Baussant, Thierry
;                   Trudel, Michel
;        TITLE OF INVENTION: PEPTIDE FRAGMENT OF RESPIRATORY
;                            SYNCYTIAL VIRUS PROTEIN G, IMMUNOGENIC AGENT,PHARMACEUTICAL
;                            COMPOSITION CONTAINING IT AND PREPARATION PROCESS
;        NUMBER OF SEQUENCES: 75
;        CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Gordon W. Hueschen
;            STREET: 715 The "H" Bldg., 310 East Michigan
;                    Avenue
;            CITY: Kalamazoo
;            STATE: MI
;            COUNTRY: USA
;            ZIP: 49007
;        COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;                      (EPO)
;        CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/091,257
;            FILING DATE: 05-Mar-2002
;            CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/08/721,979A
;            FILING DATE: October 4, 1996
;            APPLICATION NUMBER: FR 94 04009
;            FILING DATE: 06-APR-1994
;        ATTORNEY/AGENT INFORMATION:
;            NAME: Hueschen, Gordon W.
;            REGISTRATION NUMBER: 16,157
;            REFERENCE/DOCKET NUMBER: PF57PCTUS/dln
;        TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 616-382-0030
;            TELEFAX: 616-382-2030
;   INFORMATION FOR SEQ ID NO: 13:
;        SEQUENCE CHARACTERISTICS:
;            LENGTH: 1008 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;        MOLECULE TYPE: peptide
;        FEATURE:
;            NAME/KEY:  CDS
;            LOCATION: 1..1008
;            OTHER INFORMATION: /note= "name : P40"
;        SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-10-091-257-13

  Query Match             97.4%;  Score 1008;  DB 4;  Length 1008;
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  Best Local Similarity   100.0%;  Pred. No. 1.8e-276;
  Matches 1008;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         28 GCTCCGAAAGATAACACCTGGTATGCAGGTGGTAAACTGGGTTGGTCCCAGTATCACGAC 87
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GCTCCGAAAGATAACACCTGGTATGCAGGTGGTAAACTGGGTTGGTCCCAGTATCACGAC 60

Qy         88 ACCGGTTTCTACGGTAACGGTTTCCAGAACAACAACGGTCCGACCCGTAACGATCAGCTT 147
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Db         61 ACCGGTTTCTACGGTAACGGTTTCCAGAACAACAACGGTCCGACCCGTAACGATCAGCTT 120

Qy        148 GGTGCTGGTGCGTTCGGTGGTTACCAGGTTAACCCGTACCTCGGTTTCGAAATGGGTTAT 207
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGTGCTGGTGCGTTCGGTGGTTACCAGGTTAACCCGTACCTCGGTTTCGAAATGGGTTAT 180

Qy        208 GACTGGCTGGGCCGTATGGCATATAAAGGCAGCGTTGACAACGGTGCTTTCAAAGCTCAG 267
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Db        181 GACTGGCTGGGCCGTATGGCATATAAAGGCAGCGTTGACAACGGTGCTTTCAAAGCTCAG 240

Qy        268 GGCGTTCAGCTGACCGCTAAACTGGGTTACCCGATCACTGACGATCTGGACATCTACACC 327
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GGCGTTCAGCTGACCGCTAAACTGGGTTACCCGATCACTGACGATCTGGACATCTACACC 300

Qy        328 CGTCTGGGCGGCATGGTTTGGCGCGCTGACTCCAAAGGCAACTACGCTTCTACCGGCGTT 387
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Db        301 CGTCTGGGCGGCATGGTTTGGCGCGCTGACTCCAAAGGCAACTACGCTTCTACCGGCGTT 360

Qy        388 TCCCGTAGCGAACACGACACTGGCGTTTCCCCAGTATTTGCTGGCGGCGTAGAGTGGGCT 447
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TCCCGTAGCGAACACGACACTGGCGTTTCCCCAGTATTTGCTGGCGGCGTAGAGTGGGCT 420

Qy        448 GTTACTCGTGACATCGCTACCCGTCTGGAATACCAGTGGGTTAACAACATCGGCGACGCG 507
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GTTACTCGTGACATCGCTACCCGTCTGGAATACCAGTGGGTTAACAACATCGGCGACGCG 480

Qy        508 GGCACTGTGGGTACCCGTCCTGATAACGGCATGCTGAGCCTGGGCGTTTCCTACCGCTTC 567
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        568 GGTCAGGAAGATGCTGCACCGGTTGTTGCTCCGGCTCCGGCTCCGGCTCCGGAAGTGGCT 627
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Db        541 GGTCAGGAAGATGCTGCACCGGTTGTTGCTCCGGCTCCGGCTCCGGCTCCGGAAGTGGCT 600

Qy        628 ACCAAGCACTTCACCCTGAAGTCTGACGTTCTGTTCAACTTCAACAAAGCTACCCTGAAA 687
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 ACCAAGCACTTCACCCTGAAGTCTGACGTTCTGTTCAACTTCAACAAAGCTACCCTGAAA 660

Qy        688 CCGGAAGGTCAGCAGGCTCTGGATCAGCTGTACACTCAGCTGAGCAACATGGATCCGAAA 747
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Db        661 CCGGAAGGTCAGCAGGCTCTGGATCAGCTGTACACTCAGCTGAGCAACATGGATCCGAAA 720

Qy        748 GACGGTTCCGCTGTTGTTCTGGGCTACACCGACCGCATCGGTTCCGAAGCTTACAACCAG 807
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Db        721 GACGGTTCCGCTGTTGTTCTGGGCTACACCGACCGCATCGGTTCCGAAGCTTACAACCAG 780

Qy        808 CAGCTGTCTGAGAAACGTGCTCAGTCCGTTGTTGACTACCTGGTTGCTAAAGGCATCCCG 867
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Qy        868 GCTGGCAAAATCTCCGCTCGCGGCATGGGTGAATCCAACCCGGTTACTGGCAACACCTGT 927
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Qy        928 GACAACGTGAAAGCTCGCGCTGCCCTGATCGATTGCCTGGCTCCGGATCGTCGTGTAGAG 987
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Qy        988 ATCGAAGTTAAAGGCTACAAAGAAGTTGTAACTCAGCCGGCGGGTTAA 1035
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Db        961 ATCGAAGTTAAAGGCTACAAAGAAGTTGTAACTCAGCCGGCGGGTTAA 1008


RESULT 7
```

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US-08-836-500A-1
; Sequence 1, Application US/08836500A
; Patent No. 6197929
;  GENERAL INFORMATION:
;    APPLICANT:  Binz, Hans
;    APPLICANT:  Baussant, Thierry
;    APPLICANT:  Haeuw, Jean-Francois
;    APPLICANT:  Nguyen Ngoc, Thien
;    TITLE OF INVENTION:  Carrier Protein Having an Adjuvant
;    TITLE OF INVENTION:  Effect, Immunogenic Complex Containing It, Process for
;    TITLE OF INVENTION:  Their Preparation, Nucleotide Sequence and Vaccines
; Patent No. 6197929
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Rockey, Milnamow & Katz, Ltd.
;      STREET:  180 N. Stetson, 2 Prudential Plaza, Suite
;      STREET:  4700
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  U.S.A.
;      ZIP:  60601
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/836,500A
;      FILING DATE:
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Katz, Martin L.
;      REGISTRATION NUMBER:  25,011
;      REFERENCE/DOCKET NUMBER:  PIE1514P0180US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312-616-5400
;      TELEFAX:  312-616-5460
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1007 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..1007
US-08-836-500A-1

  Query Match             97.3%;  Score 1007;  DB 3;  Length 1007;
  Best Local Similarity   100.0%;  Pred. No. 3.4e-276;
  Matches 1007;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         28 GCTCCGAAAGATAACACCTGGTATGCAGGTGGTAAACTGGGTTGGTCCCAGTATCACGAC 87
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Db        481 GGCACTGTGGGTACCCGTCCTGATAACGGCATGCTGAGCCTGGGCGTTTCCTACCGCTTC 540

Qy        568 GGTCAGGAAGATGCTGCACCGGTTGTTGCTCCGGCTCCGGCTCCGGCTCCGGAAGTGGCT 627
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Db        541 GGTCAGGAAGATGCTGCACCGGTTGTTGCTCCGGCTCCGGCTCCGGCTCCGGAAGTGGCT 600

Qy        628 ACCAAGCACTTCACCCTGAAGTCTGACGTTCTGTTCAACTTCAACAAAGCTACCCTGAAA 687
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Db        601 ACCAAGCACTTCACCCTGAAGTCTGACGTTCTGTTCAACTTCAACAAAGCTACCCTGAAA 660

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Qy        748 GACGGTTCCGCTGTTGTTCTGGGCTACACCGACCGCATCGGTTCCGAAGCTTACAACCAG 807
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GACGGTTCCGCTGTTGTTCTGGGCTACACCGACCGCATCGGTTCCGAAGCTTACAACCAG 780

Qy        808 CAGCTGTCTGAGAAACGTGCTCAGTCCGTTGTTGACTACCTGGTTGCTAAAGGCATCCCG 867
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Db        781 CAGCTGTCTGAGAAACGTGCTCAGTCCGTTGTTGACTACCTGGTTGCTAAAGGCATCCCG 840

Qy        868 GCTGGCAAAATCTCCGCTCGCGGCATGGGTGAATCCAACCCGGTTACTGGCAACACCTGT 927
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Qy        988 ATCGAAGTTAAAGGCTACAAAGAAGTTGTAACTCAGCCGGCGGGTTA 1034
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RESULT 8
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; Sequence 1, Application US/09679750
; Patent No. 6780420
;   GENERAL INFORMATION:
;        APPLICANT: Binz, Hans
;                   Baussant, Thierry
;                   Haeuw, Jean-Francois
;                   Nguyen Ngoc, Thien
;        TITLE OF INVENTION: Carrier Protein Having an Adjuvant
;                            Effect, Immunogenic Complex Containing It, Process for
;                            Their Preparation, Nucleotide Sequence and Vaccines
; Patent No. 6780420
;        NUMBER OF SEQUENCES: 8
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Rockey, Milnamow & Katz, Ltd.
;             STREET: 180 N. Stetson, 2 Prudential Plaza, Suite
;                     4700
;             CITY: Chicago
;             STATE: Illinois
;             COUNTRY: U.S.A.
;             ZIP: 60601
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/679,750
;             FILING DATE: 08-Oct-2000
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/836,500
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Katz, Martin L.
;             REGISTRATION NUMBER: 25,011
;             REFERENCE/DOCKET NUMBER: PIE1514P0180US
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 312-616-5400
;             TELEFAX: 312-616-5460
;   INFORMATION FOR SEQ ID NO: 1:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 1007 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        FEATURE:
;             NAME/KEY:  CDS
;             LOCATION:  1..1007
;        SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-679-750-1

  Query Match             97.3%;  Score 1007;  DB 4;  Length 1007;
  Best Local Similarity   100.0%;  Pred. No. 3.4e-276;
  Matches 1007;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         28 GCTCCGAAAGATAACACCTGGTATGCAGGTGGTAAACTGGGTTGGTCCCAGTATCACGAC 87
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Db          1 GCTCCGAAAGATAACACCTGGTATGCAGGTGGTAAACTGGGTTGGTCCCAGTATCACGAC 60

Qy         88 ACCGGTTTCTACGGTAACGGTTTCCAGAACAACAACGGTCCGACCCGTAACGATCAGCTT 147
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Db         61 ACCGGTTTCTACGGTAACGGTTTCCAGAACAACAACGGTCCGACCCGTAACGATCAGCTT 120

Qy        148 GGTGCTGGTGCGTTCGGTGGTTACCAGGTTAACCCGTACCTCGGTTTCGAAATGGGTTAT 207
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Db        121 GGTGCTGGTGCGTTCGGTGGTTACCAGGTTAACCCGTACCTCGGTTTCGAAATGGGTTAT 180

Qy        208 GACTGGCTGGGCCGTATGGCATATAAAGGCAGCGTTGACAACGGTGCTTTCAAAGCTCAG 267
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GACTGGCTGGGCCGTATGGCATATAAAGGCAGCGTTGACAACGGTGCTTTCAAAGCTCAG 240

Qy        268 GGCGTTCAGCTGACCGCTAAACTGGGTTACCCGATCACTGACGATCTGGACATCTACACC 327
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Qy        328 CGTCTGGGCGGCATGGTTTGGCGCGCTGACTCCAAAGGCAACTACGCTTCTACCGGCGTT 387
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Db        301 CGTCTGGGCGGCATGGTTTGGCGCGCTGACTCCAAAGGCAACTACGCTTCTACCGGCGTT 360

Qy        388 TCCCGTAGCGAACACGACACTGGCGTTTCCCCAGTATTTGCTGGCGGCGTAGAGTGGGCT 447
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TCCCGTAGCGAACACGACACTGGCGTTTCCCCAGTATTTGCTGGCGGCGTAGAGTGGGCT 420

Qy        448 GTTACTCGTGACATCGCTACCCGTCTGGAATACCAGTGGGTTAACAACATCGGCGACGCG 507
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Db        421 GTTACTCGTGACATCGCTACCCGTCTGGAATACCAGTGGGTTAACAACATCGGCGACGCG 480

Qy        508 GGCACTGTGGGTACCCGTCCTGATAACGGCATGCTGAGCCTGGGCGTTTCCTACCGCTTC 567
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Db        481 GGCACTGTGGGTACCCGTCCTGATAACGGCATGCTGAGCCTGGGCGTTTCCTACCGCTTC 540

Qy        568 GGTCAGGAAGATGCTGCACCGGTTGTTGCTCCGGCTCCGGCTCCGGCTCCGGAAGTGGCT 627
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Db        541 GGTCAGGAAGATGCTGCACCGGTTGTTGCTCCGGCTCCGGCTCCGGCTCCGGAAGTGGCT 600
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Qy        628 ACCAAGCACTTCACCCTGAAGTCTGACGTTCTGTTCAACTTCAACAAAGCTACCCTGAAA 687
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Db        601 ACCAAGCACTTCACCCTGAAGTCTGACGTTCTGTTCAACTTCAACAAAGCTACCCTGAAA 660

Qy        688 CCGGAAGGTCAGCAGGCTCTGGATCAGCTGTACACTCAGCTGAGCAACATGGATCCGAAA 747
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Db        661 CCGGAAGGTCAGCAGGCTCTGGATCAGCTGTACACTCAGCTGAGCAACATGGATCCGAAA 720

Qy        748 GACGGTTCCGCTGTTGTTCTGGGCTACACCGACCGCATCGGTTCCGAAGCTTACAACCAG 807
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Db        721 GACGGTTCCGCTGTTGTTCTGGGCTACACCGACCGCATCGGTTCCGAAGCTTACAACCAG 780

Qy        808 CAGCTGTCTGAGAAACGTGCTCAGTCCGTTGTTGACTACCTGGTTGCTAAAGGCATCCCG 867
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CAGCTGTCTGAGAAACGTGCTCAGTCCGTTGTTGACTACCTGGTTGCTAAAGGCATCCCG 840

Qy        868 GCTGGCAAAATCTCCGCTCGCGGCATGGGTGAATCCAACCCGGTTACTGGCAACACCTGT 927
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GCTGGCAAAATCTCCGCTCGCGGCATGGGTGAATCCAACCCGGTTACTGGCAACACCTGT 900

Qy        928 GACAACGTGAAAGCTCGCGCTGCCCTGATCGATTGCCTGGCTCCGGATCGTCGTGTAGAG 987
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GACAACGTGAAAGCTCGCGCTGCCCTGATCGATTGCCTGGCTCCGGATCGTCGTGTAGAG 960

Qy        988 ATCGAAGTTAAAGGCTACAAAGAAGTTGTAACTCAGCCGGCGGGTTA 1034
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Db        961 ATCGAAGTTAAAGGCTACAAAGAAGTTGTAACTCAGCCGGCGGGTTA 1007
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RESULT 9
US-08-743-637B-11
; Sequence 11, Application US/08743637B
; Patent No. 5994066
;  GENERAL INFORMATION:
;    APPLICANT:  BERGERON, Michel G.
;    APPLICANT:  PICARD, Francois J.
;    APPLICANT:  OUELLETTE, Marc
;    APPLICANT:  ROY, Paul H.
;    TITLE OF INVENTION:  SPECIES-SPECIFIC AND UNIVERSAL DNA
;    TITLE OF INVENTION:  PROBES AND AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND
;    TITLE OF INVENTION:  IDENTIFY COMMON BACTERIAL PATHOGENS AND ASSOCIATED
;    TITLE OF INVENTION:  ANTIBIOTIC RESISTANCE GENES FROM CLINICAL SPECIMENS ...
;    NUMBER OF SEQUENCES:  273
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  QUARLES & BRADY
;      STREET:  411 EAST WISCONSIN AVENUE
;      CITY:  MILWAUKEE
;      STATE:  WISCONSIN
;      COUNTRY:  USA
;      ZIP:  53202-4497
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/743,637B
;      FILING DATE:  04-NOV-1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/526,840
;      FILING DATE:  11-SEP-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BAKER, Jean C.
;      REGISTRATION NUMBER:  35,433
;      REFERENCE/DOCKET NUMBER:  850586.90012
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (414) 277-5000
;      TELEFAX:  (414)277-5591
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  730 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    ORIGINAL SOURCE:
;      ORGANISM:  Klebsiella pneumoniae
US-08-743-637B-11

  Query Match             70.0%;  Score 724.4;  DB 2;  Length 730;
  Best Local Similarity   99.9%;  Pred. No. 5.2e-196;
  Matches  725;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
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Qy        276 GCTGACCGCTAAACTGGGTTACCCGATCACTGACGATCTGGACATCTACACCCGTCTGGG 335
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Db          1 GCTGACCGCTAAACTGGGTTACCCGATCACTGACGATCTGGACATCTACACCCGTCTGGG 60

Qy        336 CGGCATGGTTTGGCGCGCTGACTCCAAAGGCAACTACGCTTCTACCGGCGTTTCCCGTAG 395
              ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db         61 CGGCATGGTTTGGCGCGCTGACTCCAAAGGCAACTACGCTTCAACCGGCGTTTCCCGTAG 120

Qy        396 CGAACACGACACTGGCGTTTCCCCAGTATTTGCTGGCGGCGTAGAGTGGGCTGTTACTCG 455
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Db        121 CGAACACGACACTGGCGTTTCCCCAGTATTTGCTGGCGGCGTAGAGTGGGCTGTTACTCG 180

Qy        456 TGACATCGCTACCCGTCTGGAATACCAGTGGGTTAACAACATCGGCGACGCGGGCACTGT 515
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Db        181 TGACATCGCTACCCGTCTGGAATACCAGTGGGTTAACAACATCGGCGACGCGGGCACTGT 240

Qy        516 GGGTACCCGTCCTGATAACGGCATGCTGAGCCTGGGCGTTTCCTACCGCTTCGGTCAGGA 575
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GGGTACCCGTCCTGATAACGGCATGCTGAGCCTGGGCGTTTCCTACCGCTTCGGTCAGGA 300

Qy        576 AGATGCTGCACCGGTTGTTGCTCCGGCTCCGGCTCCGGCTCCGGAAGTGGCTACCAAGCA 635
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Db        301 AGATGCTGCACCGGTTGTTGCTCCGGCTCCGGCTCCGGCTCCGGAAGTGGCTACCAAGCA 360

Qy        636 CTTCACCCTGAAGTCTGACGTTCTGTTCAACTTCAACAAAGCTACCCTGAAACCGGAAGG 695
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CTTCACCCTGAAGTCTGACGTTCTGTTCAACTTCAACAAAGCTACCCTGAAACCGGAAGG 420

Qy        696 TCAGCAGGCTCTGGATCAGCTGTACACTCAGCTGAGCAACATGGATCCGAAAGACGGTTC 755
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCAGCAGGCTCTGGATCAGCTGTACACTCAGCTGAGCAACATGGATCCGAAAGACGGTTC 480

Qy        756 CGCTGTTGTTCTGGGCTACACCGACCGCATCGGTTCCGAAGCTTACAACCAGCAGCTGTC 815
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CGCTGTTGTTCTGGGCTACACCGACCGCATCGGTTCCGAAGCTTACAACCAGCAGCTGTC 540

Qy        816 TGAGAAACGTGCTCAGTCCGTTGTTGACTACCTGGTTGCTAAAGGCATCCCGGCTGGCAA 875
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TGAGAAACGTGCTCAGTCCGTTGTTGACTACCTGGTTGCTAAAGGCATCCCGGCTGGCAA 600

Qy        876 AATCTCCGCTCGCGGCATGGGTGAATCCAACCCGGTTACTGGCAACACCTGTGACAACGT 935
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AATCTCCGCTCGCGGCATGGGTGAATCCAACCCGGTTACTGGCAACACCTGTGACAACGT 660

Qy        936 GAAAGCTCGCGCTGCCCTGATCGATTGCCTGGCTCCGGATCGTCGTGTAGAGATCGAAGT 995
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        996 TAAAGG 1001
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Db        721 TAAAGG 726
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RESULT 10
US-08-526-840B-11
; Sequence 11, Application US/08526840B
; Patent No. 6001564
;  GENERAL INFORMATION:
;    APPLICANT:  BERGERON, Michel G.
;    APPLICANT:  OUELLETTE, Marc
;    APPLICANT:  ROY, Paul H.
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;    TITLE OF INVENTION:  SPECIFIC AND UNIVERSAL PROBES AND
;    TITLE OF INVENTION:  AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND IDENTIFY
;    TITLE OF INVENTION:  COMMON BACTERIAL PATHOGENS AND ANTIBIOTIC RESISTANCE GENES
;    TITLE OF INVENTION:  FROM CLINICAL SPECIMENS FOR ROUTINE DIAGNOSIS IN ...
;    NUMBER OF SEQUENCES:  177
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  QUARLES & BRADY
;      STREET:  411 East Wisconsin Avenue
;      CITY:  Milwaukee
;      STATE:  Wisconsin
;      COUNTRY:  USA
;      ZIP:  53202-4497
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/526,840B
;      FILING DATE:  11-SEP-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/304,732
;      FILING DATE:  12-SEP-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BAKER, Jean C.
;      REGISTRATION NUMBER:  35,433
;      REFERENCE/DOCKET NUMBER:  850586.90012
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (414) 277-5000
;      TELEFAX:  (414) 277-5591
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  730 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    ORIGINAL SOURCE:
;      ORGANISM:  Klebsiella pneumoniae
US-08-526-840B-11

  Query Match            70.0%;  Score 724.4;  DB 3;  Length 730;
  Best Local Similarity  99.9%;  Pred. No. 5.2e-196;
  Matches  725;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        276 GCTGACCGCTAAACTGGGTTACCCGATCACTGACGATCTGGACATCTACACCCGTCTGGG 335
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Qy        336 CGGCATGGTTTGGCGCGCTGACTCCAAAGGCAACTACGCTTCTACCGGCGTTTCCCGTAG 395
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Db         61 CGGCATGGTTTGGCGCGCTGACTCCAAAGGCAACTACGCTTCAACCGGCGTTTCCCGTAG 120

Qy        396 CGAACACGACACTGGCGTTTCCCCAGTATTTGCTGGCGGCGTAGAGTGGGCTGTTACTCG 455
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Db        121 CGAACACGACACTGGCGTTTCCCCAGTATTTGCTGGCGGCGTAGAGTGGGCTGTTACTCG 180

Qy        456 TGACATCGCTACCCGTCTGGAATACCAGTGGGTTAACAACATCGGCGACGCGGGCACTGT 515
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TGACATCGCTACCCGTCTGGAATACCAGTGGGTTAACAACATCGGCGACGCGGGCACTGT 240

Qy        516 GGGTACCCGTCCTGATAACGGCATGCTGAGCCTGGGCGTTTCCTACCGCTTCGGTCAGGA 575
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Db        241 GGGTACCCGTCCTGATAACGGCATGCTGAGCCTGGGCGTTTCCTACCGCTTCGGTCAGGA 300

Qy        576 AGATGCTGCACCGGTTGTTGCTCCGGCTCCGGCTCCGGCTCCGGAAGTGGCTACCAAGCA 635
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AGATGCTGCACCGGTTGTTGCTCCGGCTCCGGCTCCGGCTCCGGAAGTGGCTACCAAGCA 360

Qy        636 CTTCACCCTGAAGTCTGACGTTCTGTTCAACTTCAACAAAGCTACCCTGAAACCGGAAGG 695
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Db        361 CTTCACCCTGAAGTCTGACGTTCTGTTCAACTTCAACAAAGCTACCCTGAAACCGGAAGG 420

Qy        696 TCAGCAGGCTCTGGATCAGCTGTACACTCAGCTGAGCAACATGGATCCGAAAGACGGTTC 755
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCAGCAGGCTCTGGATCAGCTGTACACTCAGCTGAGCAACATGGATCCGAAAGACGGTTC 480

Qy        756 CGCTGTTGTTCTGGGCTACACCGACCGCATCGGTTCCGAAGCTTACAACCAGCAGCTGTC 815
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Db        481 CGCTGTTGTTCTGGGCTACACCGACCGCATCGGTTCCGAAGCTTACAACCAGCAGCTGTC 540

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Db        541 TGAGAAACGTGCTCAGTCCGTTGTTGACTACCTGGTTGCTAAAGGCATCCCGGCTGGCAA 600

Qy        876 AATCTCCGCTCGCGGCATGGGTGAATCCAACCCGGTTACTGGCAACACCTGTGACAACGT 935
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Db        601 AATCTCCGCTCGCGGCATGGGTGAATCCAACCCGGTTACTGGCAACACCTGTGACAACGT 660

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Db        661 GAAAGCTCGCGCTGCCCTGATCGATTGCCTGGCTCCGGATCGTCGTGTAGAGATCGAAGT 720

Qy        996 TAAAGG 1001
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Db        721 TAAAGG 726


RESULT 11
US-08-836-500A-3
; Sequence 3, Application US/08836500A
; Patent No. 6197929
;  GENERAL INFORMATION:
;    APPLICANT:  Binz, Hans
;    APPLICANT:  Baussant, Thierry
;    APPLICANT:  Haeuw, Jean-Francois
;    APPLICANT:  Nguyen Ngoc, Thien
;    TITLE OF INVENTION:  Carrier Protein Having an Adjuvant
;    TITLE OF INVENTION:  Effect, Immunogenic Complex Containing It, Process for
;    TITLE OF INVENTION:  Their Preparation, Nucleotide Sequence and Vaccines
; Patent No. 6197929
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Rockey, Milnamow & Katz, Ltd.
;      STREET:  180 N. Stetson, 2 Prudential Plaza, Suite
;      STREET:  4700
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  U.S.A.
;      ZIP:  60601
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/836,500A
;      FILING DATE:
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Katz, Martin L.
;      REGISTRATION NUMBER:  25,011
;      REFERENCE/DOCKET NUMBER:  PIE1514P0180US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312-616-5400
;      TELEFAX:  312-616-5460
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  537 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
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;      LOCATION:  1..537
US-08-836-500A-3

  Query Match             51.9%;  Score 537;  DB 3;  Length 537;
  Best Local Similarity   100.0%;  Pred. No. 7.5e-143;
  Matches  537;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          28 GCTCCGAAAGATAACACCTGGTATGCAGGTGGTAAACTGGGTTGGTCCCAGTATCACGAC 87
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Qy          88 ACCGGTTTCTACGGTAACGGTTTCCAGAACAACAACGGTCCGACCCGTAACGATCAGCTT 147
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Db          61 ACCGGTTTCTACGGTAACGGTTTCCAGAACAACAACGGTCCGACCCGTAACGATCAGCTT 120

Qy         148 GGTGCTGGTGCGTTCGGTGGTTACCAGGTTAACCCGTACCTCGGTTTCGAAATGGGTTAT 207
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Db         121 GGTGCTGGTGCGTTCGGTGGTTACCAGGTTAACCCGTACCTCGGTTTCGAAATGGGTTAT 180

Qy         208 GACTGGCTGGGCCGTATGGCATATAAAGGCAGCGTTGACAACGGTGCTTTCAAAGCTCAG 267
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Db         181 GACTGGCTGGGCCGTATGGCATATAAAGGCAGCGTTGACAACGGTGCTTTCAAAGCTCAG 240

Qy         268 GGCGTTCAGCTGACCGCTAAACTGGGTTACCCGATCACTGACGATCTGGACATCTACACC 327
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 GGCGTTCAGCTGACCGCTAAACTGGGTTACCCGATCACTGACGATCTGGACATCTACACC 300

Qy         328 CGTCTGGGCGGCATGGTTTGGCGCGCTGACTCCAAAGGCAACTACGCTTCTACCGGCGTT 387
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Db         301 CGTCTGGGCGGCATGGTTTGGCGCGCTGACTCCAAAGGCAACTACGCTTCTACCGGCGTT 360

Qy         388 TCCCGTAGCGAACACGACACTGGCGTTTCCCCAGTATTTGCTGGCGGCGTAGAGTGGGCT 447
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Db         361 TCCCGTAGCGAACACGACACTGGCGTTTCCCCAGTATTTGCTGGCGGCGTAGAGTGGGCT 420

Qy         448 GTTACTCGTGACATCGCTACCCGTCTGGAATACCAGTGGGTTAACAACATCGGCGACGCG 507
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Db         421 GTTACTCGTGACATCGCTACCCGTCTGGAATACCAGTGGGTTAACAACATCGGCGACGCG 480

Qy         508 GGCACTGTGGGTACCCGTCCTGATAACGGCATGCTGAGCCTGGGCGTTTCCTACCGC 564
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Db         481 GGCACTGTGGGTACCCGTCCTGATAACGGCATGCTGAGCCTGGGCGTTTCCTACCGC 537


RESULT 12
US-09-679-750-3
; Sequence 3, Application US/09679750
; Patent No. 6780420
;   GENERAL INFORMATION:
;        APPLICANT: Binz, Hans
;                   Baussant, Thierry
;                   Haeuw, Jean-Francois
;                   Nguyen Ngoc, Thien
;        TITLE OF INVENTION: Carrier Protein Having an Adjuvant
;                            Effect, Immunogenic Complex Containing It, Process for
;                            Their Preparation, Nucleotide Sequence and Vaccines
; Patent No. 6780420
;        NUMBER OF SEQUENCES: 8
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Rockey, Milnamow & Katz, Ltd.
;             STREET: 180 N. Stetson, 2 Prudential Plaza, Suite
;                     4700
;             CITY: Chicago
;             STATE: Illinois
;             COUNTRY: U.S.A.
;             ZIP: 60601
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/679,750
;             FILING DATE: 08-Oct-2000
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/836,500
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Katz, Martin L.
;             REGISTRATION NUMBER: 25,011
;             REFERENCE/DOCKET NUMBER: PIE1514P0180US
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 312-616-5400
;             TELEFAX: 312-616-5460
;   INFORMATION FOR SEQ ID NO: 3:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 537 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        FEATURE:
;             NAME/KEY:  CDS
;             LOCATION:  1..537
;        SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-679-750-3

  Query Match             51.9%;  Score 537;  DB 4;  Length 537;
  Best Local Similarity   100.0%;  Pred. No. 7.5e-143;
  Matches  537;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          28 GCTCCGAAAGATAACACCTGGTATGCAGGTGGTAAACTGGGTTGGTCCCAGTATCACGAC 87
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Qy          88 ACCGGTTTCTACGGTAACGGTTTCCAGAACAACAACGGTCCGACCCGTAACGATCAGCTT 147
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Db          61 ACCGGTTTCTACGGTAACGGTTTCCAGAACAACAACGGTCCGACCCGTAACGATCAGCTT 120

Qy         148 GGTGCTGGTGCGTTCGGTGGTTACCAGGTTAACCCGTACCTCGGTTTCGAAATGGGTTAT 207
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Db         121 GGTGCTGGTGCGTTCGGTGGTTACCAGGTTAACCCGTACCTCGGTTTCGAAATGGGTTAT 180

Qy         208 GACTGGCTGGGCCGTATGGCATATAAAGGCAGCGTTGACAACGGTGCTTTCAAAGCTCAG 267
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 GACTGGCTGGGCCGTATGGCATATAAAGGCAGCGTTGACAACGGTGCTTTCAAAGCTCAG 240

Qy         268 GGCGTTCAGCTGACCGCTAAACTGGGTTACCCGATCACTGACGATCTGGACATCTACACC 327
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Db         241 GGCGTTCAGCTGACCGCTAAACTGGGTTACCCGATCACTGACGATCTGGACATCTACACC 300

Qy         328 CGTCTGGGCGGCATGGTTTGGCGCGCTGACTCCAAAGGCAACTACGCTTCTACCGGCGTT 387
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         301 CGTCTGGGCGGCATGGTTTGGCGCGCTGACTCCAAAGGCAACTACGCTTCTACCGGCGTT 360

Qy         388 TCCCGTAGCGAACACGACACTGGCGTTTCCCCAGTATTTGCTGGCGGCGTAGAGTGGGCT 447
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         361 TCCCGTAGCGAACACGACACTGGCGTTTCCCCAGTATTTGCTGGCGGCGTAGAGTGGGCT 420

Qy         448 GTTACTCGTGACATCGCTACCCGTCTGGAATACCAGTGGGTTAACAACATCGGCGACGCG 507
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         421 GTTACTCGTGACATCGCTACCCGTCTGGAATACCAGTGGGTTAACAACATCGGCGACGCG 480

Qy         508 GGCACTGTGGGTACCCGTCCTGATAACGGCATGCTGAGCCTGGGCGTTTCCTACCGC 564
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         481 GGCACTGTGGGTACCCGTCCTGATAACGGCATGCTGAGCCTGGGCGTTTCCTACCGC 537


RESULT 13
US-09-543-681A-3750
; Sequence 3750, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
;  APPLICANT: GARY BRETON
;  TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL
```

```
;  TITLE OF INVENTION:  DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE: 2709.1002-001
;  CURRENT APPLICATION NUMBER: US/09/543,681A
;  CURRENT FILING DATE:  2000-04-05
;  PRIOR APPLICATION NUMBER: US 60/128,706
;  PRIOR FILING DATE: 1999-04-09
;  NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 3750
;   LENGTH: 1155
;   TYPE: DNA
;   ORGANISM: Proteus mirabilis
US-09-543-681A-3750

  Query Match             44.5%;  Score 460.4;  DB 4;  Length 1155;
  Best Local Similarity   67.1%;  Pred. No. 5.8e-121;
  Matches  691;  Conservative    0;  Mismatches  321;  Indels   18;  Gaps    2;

Qy         16 GTACTGAATGCGGCTCCGAAAGATAACACCTGGTATGCAGGTGGTAAACTGGGTTGGTCC 75
Db        118 GCAGCGCAAGCAGCTCCAAAAGACAATACTTGGTATACCGGTGGTAAATTAGGTTGGTCT 177

Qy         76 CAGTATCACGACACCGGTTTCTACGGTAACGGTTTCCAGAACAACAACGGTCCGACCCGT 135
Db        178 CAGTATCAAAGTACTGGTAACAATTGGGACGGCGTGAATATCGGTAACGGTAGCACACAC 237

Qy        136 AACGATCAGCTTGGTGCTGGTGCGTTCGGTGGTTACCAGGTTAACCCGTACCTCGGTTTC 195
Db        238 AAAGACCAAATTGGTGCTGGTGCATTTGCTGGTTATCAGTACAACCAATACTTAGGTTTT 297

Qy        196 GAAATGGGTTATGACTGGCTGGGCCGTATGGCATATAAAGGCAGCGTTGACAACGGTGCT 255
Db        298 GAACTGGGTTATGACTGGTTAGGTCGTATGGCTTATAAAGGTTCATACAACAACGGTGCA 357

Qy        256 TTCAAAGCTCAGGGCGTTCAGCTGACCGCTAAACTGGGTTACCCGATCACTGACGATCTG 315
Db        358 TTCAAAGCTCAAGGTATCCAATTAACCACTAAATTAAGCTATCCAGTAATGGATGACTTA 417

Qy        316 GACATCTACACCCGTCTGGGCGGCATGGTTTGGCGCGCTGACTCCAAAGGCAACTACGCT 375
Db        418 GACGTTTATACACGTTTAGGTGGTATGGTATGGCGTGCAGATTCAACTGCAACTATTAAT 477

Qy        376 TCTACCGGCGTTTCCCGT----------AGCGAACACGACACTGGCGTTTCCCCAGTA 423
Db        478 GCAACTTCAGCAGGAACTCAAAAACGTTTCTCTGAAAATGATACTGGCGTTTCTCCAGTA 537

Qy        424 TTTGCTGGCGGCGTAGAGTGGGCTGTTACTCGTGACATCGCTACCCGTCTGGAATACCAG 483
Db        538 TTCGCATTAGGTACTGAATACGCGATCACTCCTAACATTGCTACTCGTCTTGAGTATCAG 597

Qy        484 TGGGTTAACAACATCGGCGACGCGGGCACTGTGGGTACCCGTCCTGATAACGGCATGCTG 543
Db        598 TGGATCAACAACATCGGTGATAAAGGTACTCTGAACGCTCGTCCAGACAATGGTATGCTG 657

Qy        544 AGCCTGGGCGTTTCCTACCGCTTCGGTCAGGAAGATGCTGCACCGGTTGTTGCTCCGGCT 603
Db        658 AGTGTTGGTGTTGCTTACCGTTTCAACCAAGAAACTCCAGCTCCAGTTGTTGAGCCAGCT 717

Qy        604 CCG------GCTCCGGCTCCGGAAGTGGCTACCAAGCACTTCACCCTGAAGTCTGACGTT 657
Db        718 CCAGTAGTTGCTCCAGCTCCAGTTGTTGAGAACAAAACCTTTACTCTGCGTTCAGACGTT 777

Qy        658 CTGTTCAACTTCAACAAAGCTACCCTGAAACCGGAAGGTCAGCAGGCTCTGGATCAGCTG 717
Db        778 CTGTTCAACTACAACAAATCTTCTCTGAAAGCTGAAGGTCAAGAAGCACTGAATGGTCTG 837

Qy        718 TACACTCAGCTGAGCAACATGGATCCGAAAGACGGTTCCGCTGTTGTTCTGGGCTACACC 777
Db        838 TACAATGAATTAGCTAACATCGACCCAACTCAAGGTCGTGTCGTAGTTATCGGTTACACT 897

Qy        778 GACCGCATCGGTTCCGAAGCTTACAACCAGCAGCTGTCTGAGAAACGTGCTCAGTCCGTT 837
Db        898 GACCGTATCGGTTCTCAAAACTACAACCTGCCTCTGTCAGAAAAACGTGCTCAATCTGTA 957

Qy        838 GTTGACTACCTGGTTGCTAAAGGCATCCCGGCTGGCAAAATCTCCGCTCGCGGCATGGGT 897
Db        958 GTTGATTACCTGGTATCTAAAGGTATTCCTGCAAACAGCATCTCTGCAGAAGGTCGTGGT 1017

Qy        898 GAATCCAACCCGGTTACTGGCAACACCTGTGACAACGTGAAAGCTCGCGCTGCCCTGATC 957
Db       1018 AAAGAAAACCCAGTAACTGGCAACACTTGTGACAACATCAAAGCTCGTGCAGCTCTGATC 1077

Qy        958 GATTGCCTGGCTCCGGATCGTCGTGTAGAGATCGAAGTTAAAGGCTACAAAGAAGTTGTA 1017
Db       1078 GATTGCTTAGCGCCAGACCGTCGTGTAGAAATCGAAATCCAAGGTACAACTGAAGTTGTT 1137

Qy       1018 ACTCAGCCGG 1027
Db       1138 GTTCAACCTG 1147


RESULT 14
US-07-794-731A-1
; Sequence 1, Application US/07794731A
; Patent No. 5348867
;  GENERAL INFORMATION:
;    APPLICANT:  George Georgiou
;    APPLICANT:  Joseph A. Francisco
;    APPLICANT:  Charles F. Earhart
;    TITLE OF INVENTION:  Expression of Proteins on Bacterial
;    TITLE OF INVENTION:  Surface
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Arnold, White & Durkee
;      STREET:  P.O. Box 4433
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  USA
;      ZIP:  77210
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy Disk
;      COMPUTER:  IBM PC Compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/794,731A
;      FILING DATE:  19911115
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kitchell, Barbara S.
;      REGISTRATION NUMBER:  33,928
;      REFERENCE/DOCKET NUMBER:  GEOG:001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (512) 320-7200
;      TELEFAX:  (512) 474-7577
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1273 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-07-794-731A-1

  Query Match             21.7%;  Score 224.8;  DB 1;  Length 1273;
  Best Local Similarity   78.0%;  Pred. No. 4.8e-54;
  Matches  290;  Conservative    0;  Mismatches   67;  Indels   15;  Gaps    1;

Qy        176 TTAACCCGTACCTCGGTTTCGAAATGGGTTATGACTGGCTGGGCCGTATGGCATATAAAG 235
Db         92 TTAACCCGTATGTTGGCTTTGAAATGGGTTACGACTGGTTAGGTCGTATGCCGTACAAAG 151

Qy        236 GCAGCGTTGACAACGGTGCTTTCAAAGCTCAGGGCGTTCAGCTGACCGCTAAACTGGGTT 295
Db        152 GCAGCGTTGAAAACGGTGCATACAAAGCTCAGGGCGTTCAACTGACCGCTAAACTGGGTT 211

Qy        296 ACCCGATCACTGACGATCTGGACATCTACACCCGTCTGGGCGGCATGGTTTGGCGCGCTG 355
```

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Db        212 ACCCAATCACTGACGACCTGGACATCTACACTCGTCTGGGTGGCATGGTATGGCGTGCAG 271

Qy        356 ACTCCAAAGGCAACTACGCTTCTACCGGCGTTTCCCGTAGCGAACACGACACTGGCGTTT 415
              || | |||  |||                |||||   |||   | |||||||| |||||||
Db        272 ACACTAAATCCAA--------------CGTTTATGGTAAAAACCACGACACCGGCGTTT 316

Qy        416 CCCCAGTATTTGCTGGCGGCGTAGAGTGGGCTGTTACTCGTGACATCGCTACCCGTCTGG 475
              | || || |||||||| || ||||  ||  | |||| ||| ||||||||||||||||
Db        317 CTCCGGTCTTCGCTGGCGGTGTTGAGTACGCGATCACTCCTGAAATCGCTACCCGTCTGG 376

Qy        476 AATACCAGTGGGTTAACAACATCGGCGACGCGGGCACTGTGGGTACCCGTCCTGATAACG 535
              ||||||||||   |||||||||| |||||   |||  | || || ||||| || ||||
Db        377 AATACCAGTGGACCAACAACATCGGTGACGCACACACCATCGGCACTCGTCCGGACAACG 436

Qy        536 GCATGCTGAGCC 547
              | || | | | |
Db        437 GAATTCCGGGTC 448


RESULT 15
US-07-794-731A-2
; Sequence 2, Application US/07794731A
; Patent No. 5348867
;  GENERAL INFORMATION:
;    APPLICANT:  George Georgiou
;    APPLICANT:  Joseph A. Francisco
;    APPLICANT:  Charles F. Earhart
;    TITLE OF INVENTION:  Expression of Proteins on Bacterial
;    TITLE OF INVENTION:  Surface
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Arnold, White & Durkee
;      STREET:  P.O. Box 4433
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  USA
;      ZIP:  77210
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy Disk
;      COMPUTER:  IBM PC Compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/794,731A
;      FILING DATE:  19911115
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kitchell, Barbara S.
;      REGISTRATION NUMBER:  33,928
;      REFERENCE/DOCKET NUMBER:  GEOG:001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (512) 320-7200
;      TELEFAX:  (512) 474-7577
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1273 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-07-794-731A-2

  Query Match             21.7%;  Score 224.8;  DB 1;  Length 1273;
  Best Local Similarity   78.0%;  Pred. No. 4.8e-54;
  Matches  290;  Conservative    0;  Mismatches   67;  Indels   15;  Gaps    1;

Qy        176 TTAACCCGTACCTCGGTTTCGAAATGGGTTATGACTGGCTGGGCCGTATGGCATATAAAG 235
              ||||||||||  | || || |||||||||||| |||||| | || |||||| | || ||||
Db         92 TTAACCCGTATGTTGGCTTTGAAATGGGTTACGACTGGTTAGGTCGTATGCCGTACAAAG 151

Qy        236 GCAGCGTTGACAACGGTGCTTTCAAAGCTCAGGGCGTTCAGCTGACCGCTAAACTGGGTT 295
              |||||||||| |||||||| | ||||||||||||||||| ||||||||||||||||||
Db        152 GCAGCGTTGAAAACGGTGCATACAAAGCTCAGGGCGTTCAACTGACCGCTAAACTGGGTT 211

Qy        296 ACCCGATCACTGACGATCTGGACATCTACACCCGTCTGGGCGGCATGGTTTGGCGCGCTG 355
              |||| |||||||||||| |||||||||||||| |||||||| |||||||| ||||| || |
Db        212 ACCCAATCACTGACGACCTGGACATCTACACTCGTCTGGGTGGCATGGTATGGCGTGCAG 271

Qy        356 ACTCCAAAGGCAACTACGCTTCTACCGGCGTTTCCCGTAGCGAACACGACACTGGCGTTT 415
              || | |||  |||                |||||   |||   | |||||||| |||||||
Db        272 ACACTAAATCCAA--------------CGTTTATGGTAAAAACCACGACACCGGCGTTT 316

Qy        416 CCCCAGTATTTGCTGGCGGCGTAGAGTGGGCTGTTACTCGTGACATCGCTACCCGTCTGG 475
              | || || |||||||| || ||||  ||  | |||| ||| ||||||||||||||||
Db        317 CTCCGGTCTTCGCTGGCGGTGTTGAGTACGCGATCACTCCTGAAATCGCTACCCGTCTGG 376

Qy        476 AATACCAGTGGGTTAACAACATCGGCGACGCGGGCACTGTGGGTACCCGTCCTGATAACG 535
              ||||||||||   |||||||||| |||||   |||  | || || ||||| || ||||
Db        377 AATACCAGTGGACCAACAACATCGGTGACGCACACACCATCGGCACTCGTCCGGACAACG 436

Qy        536 GCATGCTGAGCC 547
              | || | | | |
Db        437 GAATTCCGGGTC 448


Search completed: January 19, 2005, 16:38:45
Job time : 122 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: January 19, 2005, 10:15:18 ; Search time 603 Seconds
(without alignments)
9010.200 Million cell updates/sec

Title: US-09-913-772-1
Perfect score: 1035
Sequence: 1 atgaaagcaatttcgtact.....taactcagccggcgggttaa 1035

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_23Sep04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1035	100.0	1035	3	AAA96568	Aaa96568 DNA encod
2	1035	100.0	1035	3	AAA63961	Aaa63961 DNA encod
3	1035	100.0	1035	3	AAA15498	Aaa15498 DNA encod
4	1035	100.0	1035	3	AAA75036	Aaa75036 cDNA enco
5	1035	100.0	1035	3	AAA75881	Aaa75881 DNA encod
6	1035	100.0	1035	3	AAA63956	Aaa63956 DNA encod
7	1035	100.0	1035	4	AAH74731	Aah74731 Nucleotid
8	1032	99.7	1032	4	AAF80152	Aaf80152 Nucleotid
9	1030.2	99.5	1035	2	AAV13868	Aav13868 Gene codi
10	1026.2	99.1	1356	4	AAF80153	Aaf80153 Nucleotid
11	1024	98.9	1032	2	AAZ30477	Aaz30477 K.pneumon
12	1024	98.9	1032	4	AAH78461	Aah78461 Nucleotid
13	1024	98.9	1032	5	AAF90077	Aaf90077 Nucleotid
14	1009.8	97.6	1158	11	ACH94485	Ach94485 Klebsiell
c 15	1009.8	97.6	1251	11	ACH94572	Ach94572 Klebsiell
16	1008	97.4	1008	2	AAV13867	Aav13867 Gene codi
17	1007	97.3	1008	2	AAT31607	Aat31607 Klebsiell
18	1006.4	97.2	1008	2	AAT03490	Aat03490 K.pneumon
19	724.4	70.0	730	2	AAT28425	Aat28425 K. pneumo
20	724.4	70.0	730	4	ABA76835	Aba76835 Klebsiell
21	681	65.8	5579	2	AAQ02032	Aaq02032 Plasmid p
22	642.4	62.1	1018	5	ADM19682	Adm19682 Novel hum
23	565	54.6	567	2	AAV13869	Aav13869 Gene codi
24	537	51.9	537	2	AAT31608	Aat31608 Klebsiell
25	486	47.0	6477	2	AAQ02030	Aaq02030 Plasmid p
26	460.4	44.5	1155	10	ADF03465	Adf03465 Bacterial
27	457.6	44.2	1107	10	ACF68624	Acf68624 Photorhab
28	457.6	44.2	110000	10	ACF67367_13	Continuation (14 o
c 29	457.6	44.2	182624	10	ACF65379	Acf65379 Photorhab
30	403	38.9	411	6	ABN83312	Abn83312 Partial O
31	303.4	29.3	3630	6	AAD40179	Aad40179 pDomp pla
32	300.6	29.0	3600	6	AAD40180	Aad40180 pEomp pla
33	298.6	28.9	3660	6	AAD40168	Aad40168 pComp pla
34	298.6	28.9	4543	6	AAD40198	Aad40198 pOHL44a p
35	224.8	21.7	1273	2	AAQ42410	Aaq42410 Tripartit
36	219	21.2	3817	10	ADD14893	Add14893 Phage dis
37	216	20.9	216	2	AAT31609	Aat31609 Klebsiell
38	161	15.6	1095	3	AAC79663	Aac79663 Virulence
39	161	15.6	1095	6	ABQ83540	Abq83540 Actinobac
40	159.4	15.4	1922	3	AAA38557	Aaa38557 Actinobac
41	159	15.4	159	2	AAT31610	Aat31610 Klebsiell
c 42	154.8	15.0	690	10	ACF65985	Acf65985 Photorhab
43	135	13.0	1035	6	ABA91422	Aba91422 Haemophil
c 44	134.2	13.0	1728	5	AAS82075	Aas82075 DNA encod
c 45	134.2	13.0	1728	5	AAS82046	Aas82046 DNA encod

ALIGNMENTS

RESULT 1
AAA96568
ID AAA96568 standard; DNA; 1035 BP.
XX
AC AAA96568;
XX
DT 08-FEB-2001 (first entry)
XX
DE DNA encoding a P40 polypeptide of Klebsiella pneumoniae.
XX
KW P40; membrane fraction; Gram-negative bacteria; anticancer;
KW immune response; mononuclear blood cell; tumour necrosis factor-alpha;
KW interleukin-12; antitumour; cancer; ss.
XX
OS Klebsiella pneumoniae.
XX
FH Key Location/Qualifiers
FT CDS 1. .1035
FT /*tag= a
FT /product= "P40"
XX
PN WO200054790-A1.
XX
PD 21-SEP-2000.
XX
PF 15-MAR-2000; 2000WO-FR000623.
XX
PR 15-MAR-1999; 99FR-00003154.
XX
PA (FABR) FABRE MEDICAMENT SA PIERRE.
XX
PI Libon C, Corvaia N, Beck A, Bonnefoy J;
XX
DR WPI; 2000-587477/55.
DR P-PSDB; AAB18994.
XX
PT Use of membrane fractions from Gram-negative bacteria as immunostimulants
PT for the treatment or prevention of cancer, increases effect of e.g.
PT chemotherapeutic agents.
XX
PS Disclosure; Page 25-27; 34pp; French.
XX
CC The present sequence encodes a P40 polypeptide of Klebsiella pneumoniae.
CC The protein is found in the membrane fraction, and is used in the method

```
CC   of the invention. The specification describes the use of a membrane
CC   fraction from Gram-negative bacteria for the preparation of an
CC   immunostimulating composition that can induce an anticancer immune
CC   response. The membrane fraction not only stimulates proliferation of
CC   human mononuclear blood cells (immunostimulation) but also induces
CC   production of tumour necrosis factor-alpha and interleukin (IL)-12, which
CC   are known to have antitumour activity, so that it improves the effects of
CC   other co-administered anticancer treatments (chemotherapy or radiation).
CC   The membrane fraction is used for treatment and prevention of cancer
CC   (particularly of the bladder, prostate, colon or liver) and also
CC   malignant melanomas
XX
SQ   Sequence 1035 BP; 227 A; 283 C; 288 G; 237 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 1035;  DB 3;  Length 1035;
  Best Local Similarity   100.0%;  Pred. No. 3.5e-283;
  Matches 1035;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGAAAGCAATTTTCGTACTGAATGCGGCTCCGAAAGATAACACCTGGTATGCAGGTGGT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGAAAGCAATTTTCGTACTGAATGCGGCTCCGAAAGATAACACCTGGTATGCAGGTGGT 60

Qy         61 AAACTGGGTTGGTCCCAGTATCACGACACCGGTTTCTACGGTAACGGTTTCCAGAACAAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AAACTGGGTTGGTCCCAGTATCACGACACCGGTTTCTACGGTAACGGTTTCCAGAACAAC 120

Qy        121 AACGGTCCGACCCGTAACGATCAGCTTGGTGCTGGTGCGTTCGGTGGTTACCAGGTTAAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AACGGTCCGACCCGTAACGATCAGCTTGGTGCTGGTGCGTTCGGTGGTTACCAGGTTAAC 180

Qy        181 CCGTACCTCGGTTTCGAAATGGGTTATGACTGGCTGGGCCGTATGGCATATAAAGGCAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CCGTACCTCGGTTTCGAAATGGGTTATGACTGGCTGGGCCGTATGGCATATAAAGGCAGC 240

Qy        241 GTTGACAACGGTGCTTTCAAAGCTCAGGGCGTTCAGCTGACCGCTAAACTGGGTTACCCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GTTGACAACGGTGCTTTCAAAGCTCAGGGCGTTCAGCTGACCGCTAAACTGGGTTACCCG 300

Qy        301 ATCACTGACGATCTGGACATCTACACCCGTCTGGGCGGCATGGTTTGGCGCGCTGACTCC 360
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Db        301 ATCACTGACGATCTGGACATCTACACCCGTCTGGGCGGCATGGTTTGGCGCGCTGACTCC 360

Qy        361 AAAGGCAACTACGCTTCTACCGGCGTTTCCCGTAGCGAACACGACACTGGCGTTTCCCCA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGGCAACTACGCTTCTACCGGCGTTTCCCGTAGCGAACACGACACTGGCGTTTCCCCA 420

Qy        421 GTATTTGCTGGCGGCGTAGAGTGGGCTGTTACTCGTGACATCGCTACCCGTCTGGAATAC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GTATTTGCTGGCGGCGTAGAGTGGGCTGTTACTCGTGACATCGCTACCCGTCTGGAATAC 480

Qy        481 CAGTGGGTTAACAACATCGGCGACGCGGGCACTGTGGGTACCCGTCCTGATAACGGCATG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CAGTGGGTTAACAACATCGGCGACGCGGGCACTGTGGGTACCCGTCCTGATAACGGCATG 540

Qy        541 CTGAGCCTGGGCGTTTCCTACCGCTTCGGTCAGGAAGATGCTGCACCGGTTGTTGCTCCG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CTGAGCCTGGGCGTTTCCTACCGCTTCGGTCAGGAAGATGCTGCACCGGTTGTTGCTCCG 600

Qy        601 GCTCCGGCTCCGGCTCCGGAAGTGGCTACCAAGCACTTCACCCTGAAGTCTGACGTTCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GCTCCGGCTCCGGCTCCGGAAGTGGCTACCAAGCACTTCACCCTGAAGTCTGACGTTCTG 660

Qy        661 TTCAACTTCAACAAAGCTACCCTGAAACCGGAAGGTCAGCAGGCTCTGGATCAGCTGTAC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TTCAACTTCAACAAAGCTACCCTGAAACCGGAAGGTCAGCAGGCTCTGGATCAGCTGTAC 720

Qy        721 ACTCAGCTGAGCAACATGGATCCGAAAGACGGTTCCGCTGTTGTTCTGGGCTACACCGAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ACTCAGCTGAGCAACATGGATCCGAAAGACGGTTCCGCTGTTGTTCTGGGCTACACCGAC 780

Qy        781 CGCATCGGTTCCGAAGCTTACAACCAGCAGCTGTCTGAGAAACGTGCTCAGTCCGTTGTT 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CGCATCGGTTCCGAAGCTTACAACCAGCAGCTGTCTGAGAAACGTGCTCAGTCCGTTGTT 840

Qy        841 GACTACCTGGTTGCTAAAGGCATCCCGGCTGGCAAAATCTCCGCTCGCGGCATGGGTGAA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GACTACCTGGTTGCTAAAGGCATCCCGGCTGGCAAAATCTCCGCTCGCGGCATGGGTGAA 900

Qy        901 TCCAACCCGGTTACTGGCAACACCTGTGACAACGTGAAAGCTCGCGCTGCCCTGATCGAT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TCCAACCCGGTTACTGGCAACACCTGTGACAACGTGAAAGCTCGCGCTGCCCTGATCGAT 960

Qy        961 TGCCTGGCTCCGGATCGTCGTGTAGAGATCGAAGTTAAAGGCTACAAAGAAGTTGTAACT 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TGCCTGGCTCCGGATCGTCGTGTAGAGATCGAAGTTAAAGGCTACAAAGAAGTTGTAACT 1020

Qy       1021 CAGCCGGCGGGTTAA 1035
              |||||||||||||||
Db       1021 CAGCCGGCGGGTTAA 1035


RESULT 2
AAA63961
ID   AAA63961 standard; DNA; 1035 BP.
XX
AC   AAA63961;
XX
DT   04-DEC-2000  (first entry)
XX
DE   DNA encoding an outer membrane protein A (OmpA), designated P40.
XX
KW   Outer membrane protein A; OmpA; P40; cytotoxic T cell response;
KW   CTL response; tumour cell; vaccine; infection; tumour; melanoma;
KW   genetic vaccine; ss.
XX
OS   Klebsiella pneumoniae.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1035
FT                   /*tag=  a
FT                   /product= "outer membrane protein A (OmpA) P40"
XX
PN   WO200048628-A1.
XX
PD   24-AUG-2000.
XX
PF   17-FEB-2000; 2000WO-FR000393.
XX
PR   17-FEB-1999;   99FR-00001917.
XX
PA   (FABR ) FABRE MEDICAMENT SA PIERRE.
XX
PI   Renno T,  Bonnefoy J;
XX
DR   WPI; 2000-543667/49.
DR   P-PSDB; AAB08317.
XX
PT   Use of enterobacterial outer membrane protein A in vaccines for inducing
PT   cytotoxic T cell responses, useful for treating or preventing infections
PT   and tumors.
XX
PS   Claim 24; Page 36-37; 45pp; French.
XX
CC   The present sequence encodes a Klebsiella pneumoniae outer membrane
CC   protein A (OmpA), designated P40. The enterobacterial OmpA polypeptide,
CC   or its fragments, is used for preparing a composition that induces, or
CC   increases, the cytotoxic T cell (CTL) response against an infectious
CC   agent or tumour cell. Compositions containing OmpA, optionally mixed with
CC   or coupled to a suitable antigen or hapten, are used as vaccines for
CC   treatment or prevention of infections caused by viruses, bacteria, fungi
CC   and parasites or tumors, particularly where associated with an antigen
CC   and specifically melanoma. Nucleic acids that encode OmpA (or its fusion
CC   with antigens or haptens) are useful as genetic vaccines again for
CC   treating infections and tumors
XX
SQ   Sequence 1035 BP; 227 A; 283 C; 288 G; 237 T; 0 U; 0 Other;
```

```
  Query Match           100.0%;  Score 1035;  DB 3;  Length 1035;
  Best Local Similarity  100.0%;  Pred. No. 3.5e-283;
  Matches 1035;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGAAAGCAATTTTCGTACTGAATGCGGCTCCGAAAGATAACACCTGGTATGCAGGTGGT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGAAAGCAATTTTCGTACTGAATGCGGCTCCGAAAGATAACACCTGGTATGCAGGTGGT 60

Qy         61 AAACTGGGTTGGTCCCAGTATCACGACACCGGTTTCTACGGTAACGGTTTCCAGAACAAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AAACTGGGTTGGTCCCAGTATCACGACACCGGTTTCTACGGTAACGGTTTCCAGAACAAC 120

Qy        121 AACGGTCCGACCCGTAACGATCAGCTTGGTGCTGGTGCGTTCGGTGGTTACCAGGTTAAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AACGGTCCGACCCGTAACGATCAGCTTGGTGCTGGTGCGTTCGGTGGTTACCAGGTTAAC 180

Qy        181 CCGTACCTCGGTTTCGAAATGGGTTATGACTGGCTGGGCCGTATGGCATATAAAGGCAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CCGTACCTCGGTTTCGAAATGGGTTATGACTGGCTGGGCCGTATGGCATATAAAGGCAGC 240

Qy        241 GTTGACAACGGTGCTTTCAAAGCTCAGGGCGTTCAGCTGACCGCTAAACTGGGTTACCCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GTTGACAACGGTGCTTTCAAAGCTCAGGGCGTTCAGCTGACCGCTAAACTGGGTTACCCG 300

Qy        301 ATCACTGACGATCTGGACATCTACACCCGTCTGGGCGGCATGGTTTGGCGCGCTGACTCC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ATCACTGACGATCTGGACATCTACACCCGTCTGGGCGGCATGGTTTGGCGCGCTGACTCC 360

Qy        361 AAAGGCAACTACGCTTCTACCGGCGTTTCCCGTAGCGAACACGACACTGGCGTTTCCCCA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGGCAACTACGCTTCTACCGGCGTTTCCCGTAGCGAACACGACACTGGCGTTTCCCCA 420

Qy        421 GTATTTGCTGGCGGCGTAGAGTGGGCTGTTACTCGTGACATCGCTACCCGTCTGGAATAC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GTATTTGCTGGCGGCGTAGAGTGGGCTGTTACTCGTGACATCGCTACCCGTCTGGAATAC 480

Qy        481 CAGTGGGTTAACAACATCGGCGACGCGGGCACTGTGGGTACCCGTCCTGATAACGGCATG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CAGTGGGTTAACAACATCGGCGACGCGGGCACTGTGGGTACCCGTCCTGATAACGGCATG 540

Qy        541 CTGAGCCTGGGCGTTTCCTACCGCTTCGGTCAGGAAGATGCTGCACCGGTTGTTGCTCCG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CTGAGCCTGGGCGTTTCCTACCGCTTCGGTCAGGAAGATGCTGCACCGGTTGTTGCTCCG 600

Qy        601 GCTCCGGCTCCGGCTCCGGAAGTGGCTACCAAGCACTTCACCCTGAAGTCTGACGTTCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GCTCCGGCTCCGGCTCCGGAAGTGGCTACCAAGCACTTCACCCTGAAGTCTGACGTTCTG 660

Qy        661 TTCAACTTCAACAAAGCTACCCTGAAACCGGAAGGTCAGCAGGCTCTGGATCAGCTGTAC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TTCAACTTCAACAAAGCTACCCTGAAACCGGAAGGTCAGCAGGCTCTGGATCAGCTGTAC 720

Qy        721 ACTCAGCTGAGCAACATGGATCCGAAAGACGGTTCCGCTGTTGTTCTGGGCTACACCGAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ACTCAGCTGAGCAACATGGATCCGAAAGACGGTTCCGCTGTTGTTCTGGGCTACACCGAC 780

Qy        781 CGCATCGGTTCCGAAGCTTACAACCAGCAGCTGTCTGAGAAACGTGCTCAGTCCGTTGTT 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CGCATCGGTTCCGAAGCTTACAACCAGCAGCTGTCTGAGAAACGTGCTCAGTCCGTTGTT 840

Qy        841 GACTACCTGGTTGCTAAAGGCATCCCGGCTGGCAAAATCTCCGCTCGCGGCATGGGTGAA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GACTACCTGGTTGCTAAAGGCATCCCGGCTGGCAAAATCTCCGCTCGCGGCATGGGTGAA 900

Qy        901 TCCAACCCGGTTACTGGCAACACCTGTGACAACGTGAAAGCTCGCGCTGCCCTGATCGAT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TCCAACCCGGTTACTGGCAACACCTGTGACAACGTGAAAGCTCGCGCTGCCCTGATCGAT 960

Qy        961 TGCCTGGCTCCGGATCGTCGTGTAGAGATCGAAGTTAAAGGCTACAAAGAAGTTGTAACT 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TGCCTGGCTCCGGATCGTCGTGTAGAGATCGAAGTTAAAGGCTACAAAGAAGTTGTAACT 1020

Qy       1021 CAGCCGGCGGGTTAA 1035
              |||||||||||||||
Db       1021 CAGCCGGCGGGTTAA 1035
```

```
RESULT 3
AAA15498
ID   AAA15498 standard; DNA; 1035 BP.
XX
AC   AAA15498;
XX
DT   04-SEP-2000  (first entry)
XX
DE   DNA encoding a Klebsiella P40 protein.
XX
KW   P40 protein; outer membrane protein A; OmpA; antigen-presenting cell;
KW   dendritic cell; antigen delivery; immune response; cancer;
KW   tumour-associated antigen; autoimmune disease; allergy; graft rejection;
KW   cardiovascular disease; central nervous system disease; inflammation;
KW   infection; immune deficiency; ss.
XX
OS   Klebsiella pneumoniae.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1035
FT                   /*tag=  a
FT                   /product= "P40 protein"
XX
PN   WO200027432-A1.
XX
PD   18-MAY-2000.
XX
PF   08-NOV-1999;   99WO-FR002734.
XX
PR   06-NOV-1998;   98FR-00014007.
XX
PA   (FABR ) FABRE MEDICAMENT SA PIERRE.
XX
PI   Bonnefoy J,  Lecoanet S,  Aubry J,  Jeannin P,  Baussant T;
XX
DR   WPI; 2000-387342/33.
DR   P-PSDB; AAY93341.
XX
PT   Use of enterobacterial outer membrane protein A for delivering active
PT   substances, particularly immunogens for treating or preventing e.g.
PT   cancer, to antigen presenting cells.
XX
PS   Example 1; Page 26-28; 35pp; French.
XX
CC   The present sequence encodes a P40 protein. The protein is an outer
CC   membrane protein A (OmpA). The protein is used in pharmaceutical
CC   compositions for specific targeting of an active substance to antigen-
CC   presenting cells (APCs), especially dendritic cells. OmpA binds
CC   specifically to APCs and is internalised by them (in contrast to other
CC   protein carriers such as tetanus toxoid). The OmpA protein is used to
CC   deliver an antigen or hapten to modify (specifically to improve) an
CC   immune response, especially for treatment or prevention of cancers
CC   (particularly those that express a associated-associated antigen),
CC   autoimmune disease, allergy, graft rejection, cardiovascular or central
CC   nervous system diseases, inflammation, infection or immune deficiency
XX
SQ   Sequence 1035 BP; 227 A; 283 C; 288 G; 237 T; 0 U; 0 Other;
```

```
  Query Match           100.0%;  Score 1035;  DB 3;  Length 1035;
  Best Local Similarity  100.0%;  Pred. No. 3.5e-283;
  Matches 1035;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGAAAGCAATTTTCGTACTGAATGCGGCTCCGAAAGATAACACCTGGTATGCAGGTGGT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGAAAGCAATTTTCGTACTGAATGCGGCTCCGAAAGATAACACCTGGTATGCAGGTGGT 60

Qy         61 AAACTGGGTTGGTCCCAGTATCACGACACCGGTTTCTACGGTAACGGTTTCCAGAACAAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db         61 AAACTGGGTTGGTCCCAGTATCACGACACCGGTTTCTACGGTAACGGTTTCCAGAACAAC 120

Qy        121 AACGGTCCGACCCGTAACGATCAGCTTGGTGCTGGTGCGTTCGGTGGTTACCAGGTTAAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AACGGTCCGACCCGTAACGATCAGCTTGGTGCTGGTGCGTTCGGTGGTTACCAGGTTAAC 180

Qy        181 CCGTACCTCGGTTTCGAAATGGGTTATGACTGGCTGGGCCGTATGGCATATAAAGGCAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CCGTACCTCGGTTTCGAAATGGGTTATGACTGGCTGGGCCGTATGGCATATAAAGGCAGC 240

Qy        241 GTTGACAACGGTGCTTTCAAAGCTCAGGGCGTTCAGCTGACCGCTAAACTGGGTTACCCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GTTGACAACGGTGCTTTCAAAGCTCAGGGCGTTCAGCTGACCGCTAAACTGGGTTACCCG 300

Qy        301 ATCACTGACGATCTGGACATCTACACCCGTCTGGGCGGCATGGTTTGGCGCGCTGACTCC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ATCACTGACGATCTGGACATCTACACCCGTCTGGGCGGCATGGTTTGGCGCGCTGACTCC 360

Qy        361 AAAGGCAACTACGCTTCTACCGGCGTTTCCCGTAGCGAACACGACACTGGCGTTTCCCCA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGGCAACTACGCTTCTACCGGCGTTTCCCGTAGCGAACACGACACTGGCGTTTCCCCA 420

Qy        421 GTATTTGCTGGCGGCGTAGAGTGGGCTGTTACTCGTGACATCGCTACCCGTCTGGAATAC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GTATTTGCTGGCGGCGTAGAGTGGGCTGTTACTCGTGACATCGCTACCCGTCTGGAATAC 480

Qy        481 CAGTGGGTTAACAACATCGGCGACGCGGGCACTGTGGGTACCCGTCCTGATAACGGCATG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CAGTGGGTTAACAACATCGGCGACGCGGGCACTGTGGGTACCCGTCCTGATAACGGCATG 540

Qy        541 CTGAGCCTGGGCGTTTCCTACCGCTTCGGTCAGGAAGATGCTGCACCGGTTGTTGCTCCG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CTGAGCCTGGGCGTTTCCTACCGCTTCGGTCAGGAAGATGCTGCACCGGTTGTTGCTCCG 600

Qy        601 GCTCCGGCTCCGGCTCCGGAAGTGGCTACCAAGCACTTCACCCTGAAGTCTGACGTTCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GCTCCGGCTCCGGCTCCGGAAGTGGCTACCAAGCACTTCACCCTGAAGTCTGACGTTCTG 660

Qy        661 TTCAACTTCAACAAAGCTACCCTGAAACCGGAAGGTCAGCAGGCTCTGGATCAGCTGTAC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TTCAACTTCAACAAAGCTACCCTGAAACCGGAAGGTCAGCAGGCTCTGGATCAGCTGTAC 720

Qy        721 ACTCAGCTGAGCAACATGGATCCGAAAGACGGTTCCGCTGTTGTTCTGGGCTACACCGAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ACTCAGCTGAGCAACATGGATCCGAAAGACGGTTCCGCTGTTGTTCTGGGCTACACCGAC 780

Qy        781 CGCATCGGTTCCGAAGCTTACAACCAGCAGCTGTCTGAGAAACGTGCTCAGTCCGTTGTT 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CGCATCGGTTCCGAAGCTTACAACCAGCAGCTGTCTGAGAAACGTGCTCAGTCCGTTGTT 840

Qy        841 GACTACCTGGTTGCTAAAGGCATCCCGGCTGGCAAAATCTCCGCTCGCGGCATGGGTGAA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GACTACCTGGTTGCTAAAGGCATCCCGGCTGGCAAAATCTCCGCTCGCGGCATGGGTGAA 900

Qy        901 TCCAACCCGGTTACTGGCAACACCTGTGACAACGTGAAAGCTCGCGCTGCCCTGATCGAT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TCCAACCCGGTTACTGGCAACACCTGTGACAACGTGAAAGCTCGCGCTGCCCTGATCGAT 960

Qy        961 TGCCTGGCTCCGGATCGTCGTGTAGAGATCGAAGTTAAAGGCTACAAAGAAGTTGTAACT 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TGCCTGGCTCCGGATCGTCGTGTAGAGATCGAAGTTAAAGGCTACAAAGAAGTTGTAACT 1020

Qy       1021 CAGCCGGCGGGTTAA 1035
              |||||||||||||||
Db       1021 CAGCCGGCGGGTTAA 1035


RESULT 4
AAA75036
ID   AAA75036 standard; cDNA; 1035 BP.
XX
AC   AAA75036;
XX
```

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DT   02-JAN-2001  (first entry)
XX
DE   cDNA encoding a P40 polypeptide (an outer membrane protein A (OmpA)).
XX
KW   P40; outer membrane protein A; OmpA; immunogen; cytokine; growth factor;
KW   hormone; tumour-specific marker; vaccine; cancer; contraceptive; ss.
XX
OS   Klebsiella pneumoniae.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1035
FT                   /*tag=  a
FT                   /product= "P40"
XX
PN   FR2789902-A1.
XX
PD   25-AUG-2000.
XX
PF   24-FEB-1999;   99FR-00002314.
XX
PR   24-FEB-1999;   99FR-00002314.
XX
PA   (FABR ) FABRE MEDICAMENT SA PIERRE.
XX
PI   Goetsch L,  Corvaia N,  Beck A,  Haeuw JF,  Bonnefoy JY;
XX
DR   WPI; 2000-573921/54.
DR   P-PSDB; AAB08825.
XX
PT   Use of enterobacterial outer membrane protein as immunogenic carrier,
PT   particularly for contraceptive and anti-cancer vaccines, provides strong
PT   humoral response.
XX
PS   Claim 14; Page 21-22; 34pp; French.
XX
CC   The present sequence encodes a P40 polypeptide of Klebsiella pneumoniae.
CC   P40 is an enterobacterial outer membrane protein A (OmpA). It can be
CC   associated an immunogen, and used to prepare a pharmaceutical composition
CC   for improving the immunological response to the immunogen. The immunogen
CC   is selected from cytokines, growth factors or hormones (or their
CC   receptors) and/or tumour-specific markers. Compositions containing OmpA
CC   induce a strong and specific antibody response. The compositions of the
CC   invention are especially useful in vaccines to prevent or treat cancer or
CC   as contraceptives
XX
SQ   Sequence 1035 BP; 227 A; 283 C; 288 G; 237 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 1035;  DB 3;  Length 1035;
  Best Local Similarity   100.0%;  Pred. No. 3.5e-283;
  Matches 1035;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGAAAGCAATTTTCGTACTGAATGCGGCTCCGAAAGATAACACCTGGTATGCAGGTGGT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGAAAGCAATTTTCGTACTGAATGCGGCTCCGAAAGATAACACCTGGTATGCAGGTGGT 60

Qy         61 AAACTGGGTTGGTCCCAGTATCACGACACCGGTTTCTACGGTAACGGTTTCCAGAACAAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AAACTGGGTTGGTCCCAGTATCACGACACCGGTTTCTACGGTAACGGTTTCCAGAACAAC 120

Qy        121 AACGGTCCGACCCGTAACGATCAGCTTGGTGCTGGTGCGTTCGGTGGTTACCAGGTTAAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AACGGTCCGACCCGTAACGATCAGCTTGGTGCTGGTGCGTTCGGTGGTTACCAGGTTAAC 180

Qy        181 CCGTACCTCGGTTTCGAAATGGGTTATGACTGGCTGGGCCGTATGGCATATAAAGGCAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CCGTACCTCGGTTTCGAAATGGGTTATGACTGGCTGGGCCGTATGGCATATAAAGGCAGC 240

Qy        241 GTTGACAACGGTGCTTTCAAAGCTCAGGGCGTTCAGCTGACCGCTAAACTGGGTTACCCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GTTGACAACGGTGCTTTCAAAGCTCAGGGCGTTCAGCTGACCGCTAAACTGGGTTACCCG 300

Qy        301 ATCACTGACGATCTGGACATCTACACCCGTCTGGGCGGCATGGTTTGGCGCGCTGACTCC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        301 ATCACTGACGATCTGGACATCTACACCCGTCTGGGCGGCATGGTTTGGCGCGCTGACTCC 360

Qy        361 AAAGGCAACTACGCTTCTACCGGCGTTTCCCGTAGCGAACACGACACTGGCGTTTCCCCA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGGCAACTACGCTTCTACCGGCGTTTCCCGTAGCGAACACGACACTGGCGTTTCCCCA 420

Qy        421 GTATTTGCTGGCGGCGTAGAGTGGGCTGTTACTCGTGACATCGCTACCCGTCTGGAATAC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GTATTTGCTGGCGGCGTAGAGTGGGCTGTTACTCGTGACATCGCTACCCGTCTGGAATAC 480

Qy        481 CAGTGGGTTAACAACATCGGCGACGCGGGCACTGTGGGTACCCGTCCTGATAACGGCATG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CAGTGGGTTAACAACATCGGCGACGCGGGCACTGTGGGTACCCGTCCTGATAACGGCATG 540

Qy        541 CTGAGCCTGGGCGTTTCCTACCGCTTCGGTCAGGAAGATGCTGCACCGGTTGTTGCTCCG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CTGAGCCTGGGCGTTTCCTACCGCTTCGGTCAGGAAGATGCTGCACCGGTTGTTGCTCCG 600

Qy        601 GCTCCGGCTCCGGCTCCGGAAGTGGCTACCAAGCACTTCACCCTGAAGTCTGACGTTCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GCTCCGGCTCCGGCTCCGGAAGTGGCTACCAAGCACTTCACCCTGAAGTCTGACGTTCTG 660

Qy        661 TTCAACTTCAACAAAGCTACCCTGAAACCGGAAGGTCAGCAGGCTCTGGATCAGCTGTAC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TTCAACTTCAACAAAGCTACCCTGAAACCGGAAGGTCAGCAGGCTCTGGATCAGCTGTAC 720

Qy        721 ACTCAGCTGAGCAACATGGATCCGAAAGACGGTTCCGCTGTTGTTCTGGGCTACACCGAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ACTCAGCTGAGCAACATGGATCCGAAAGACGGTTCCGCTGTTGTTCTGGGCTACACCGAC 780

Qy        781 CGCATCGGTTCCGAAGCTTACAACCAGCAGCTGTCTGAGAAACGTGCTCAGTCCGTTGTT 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CGCATCGGTTCCGAAGCTTACAACCAGCAGCTGTCTGAGAAACGTGCTCAGTCCGTTGTT 840

Qy        841 GACTACCTGGTTGCTAAAGGCATCCCGGCTGGCAAAATCTCCGCTCGCGGCATGGGTGAA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GACTACCTGGTTGCTAAAGGCATCCCGGCTGGCAAAATCTCCGCTCGCGGCATGGGTGAA 900

Qy        901 TCCAACCCGGTTACTGGCAACACCTGTGACAACGTGAAAGCTCGCGCTGCCCTGATCGAT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TCCAACCCGGTTACTGGCAACACCTGTGACAACGTGAAAGCTCGCGCTGCCCTGATCGAT 960

Qy        961 TGCCTGGCTCCGGATCGTCGTGTAGAGATCGAAGTTAAAGGCTACAAAGAAGTTGTAACT 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TGCCTGGCTCCGGATCGTCGTGTAGAGATCGAAGTTAAAGGCTACAAAGAAGTTGTAACT 1020

Qy       1021 CAGCCGGCGGGTTAA 1035
              |||||||||||||||
Db       1021 CAGCCGGCGGGTTAA 1035
```

RESULT 5
AAA75881
ID AAA75881 standard; DNA; 1035 BP.
XX
AC AAA75881;
XX
DT 22-JAN-2001 (first entry)
XX
DE DNA encoding a Klebsiella pneumoniae P40 polypeptide.
XX
KW P40 polypeptide; membrane fraction; antigen; hapten; immune response;
KW infectious disease; cancer; paramyxoviruse infection;
KW respiratory syncytial virus; parainfluenza; ss.
XX
OS Klebsiella pneumoniae.
XX
FH Key   Location/Qualifiers
FT CDS   1. .1035
FT   /*tag= a
FT   /product= "P40 polypeptide"
XX
PN WO200054789-A1.
XX
PD 21-SEP-2000.
XX
PF 15-MAR-2000; 2000WO-FR000622.
XX
PR 15-MAR-1999; 99FR-00003153.
XX
PA (FABR) FABRE MEDICAMENT SA PIERRE.
XX
PI Libon C, Corvaia N, N'guyen TN, Beck A, Bonnefoy J;
XX
DR WPI; 2000-587476/55.
DR P-PSDB; AAB18804.
XX
PT Use of Klebsiella membrane fraction as adjuvant, for e.g. antitumor or
PT antiviral vaccines, to direct a Th1, or mixed, immune response against
PT associated antigen.
XX
PS Disclosure; Page 27-29; 36pp; French.
XX
CC The present sequence encodes a Klebsiella pneumoniae P40 polypeptide. The
CC protein is isolated from a membrane fraction. The specification describes
CC the use of a membrane fraction from Klebsiella pneumoniae, associated
CC with an antigen or hapten, for preparation of a pharmaceutical
CC composition that directs a Th1, or mixed Th1/Th2 immune response. The
CC composition is used for treatment or prevention of infectious diseases
CC (viral, bacterial, fungal or parasitic) or cancers, most especially
CC infections by paramyxoviruses, specifically respiratory syncytial virus
CC or parainfluenza
XX
SQ Sequence 1035 BP; 227 A; 283 C; 288 G; 237 T; 0 U; 0 Other;

  Query Match   100.0%; Score 1035; DB 3; Length 1035;
  Best Local Similarity   100.0%; Pred. No. 3.5e-283;
  Matches 1035; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Qy          1 ATGAAAGCAATTTTCGTACTGAATGCGGCTCCGAAAGATAACACCTGGTATGCAGGTGGT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGAAAGCAATTTTCGTACTGAATGCGGCTCCGAAAGATAACACCTGGTATGCAGGTGGT 60

Qy         61 AAACTGGGTTGGTCCCAGTATCACGACACCGGTTTCTACGGTAACGGTTTCCAGAACAAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AAACTGGGTTGGTCCCAGTATCACGACACCGGTTTCTACGGTAACGGTTTCCAGAACAAC 120

Qy        121 AACGGTCCGACCCGTAACGATCAGCTTGGTGCTGGTGCGTTCGGTGGTTACCAGGTTAAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AACGGTCCGACCCGTAACGATCAGCTTGGTGCTGGTGCGTTCGGTGGTTACCAGGTTAAC 180

Qy        181 CCGTACCTCGGTTTCGAAATGGGTTATGACTGGCTGGGCCGTATGGCATATAAAGGCAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CCGTACCTCGGTTTCGAAATGGGTTATGACTGGCTGGGCCGTATGGCATATAAAGGCAGC 240

Qy        241 GTTGACAACGGTGCTTTCAAAGCTCAGGGCGTTCAGCTGACCGCTAAACTGGGTTACCCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GTTGACAACGGTGCTTTCAAAGCTCAGGGCGTTCAGCTGACCGCTAAACTGGGTTACCCG 300

Qy        301 ATCACTGACGATCTGGACATCTACACCCGTCTGGGCGGCATGGTTTGGCGCGCTGACTCC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ATCACTGACGATCTGGACATCTACACCCGTCTGGGCGGCATGGTTTGGCGCGCTGACTCC 360

Qy        361 AAAGGCAACTACGCTTCTACCGGCGTTTCCCGTAGCGAACACGACACTGGCGTTTCCCCA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGGCAACTACGCTTCTACCGGCGTTTCCCGTAGCGAACACGACACTGGCGTTTCCCCA 420

Qy        421 GTATTTGCTGGCGGCGTAGAGTGGGCTGTTACTCGTGACATCGCTACCCGTCTGGAATAC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GTATTTGCTGGCGGCGTAGAGTGGGCTGTTACTCGTGACATCGCTACCCGTCTGGAATAC 480

Qy        481 CAGTGGGTTAACAACATCGGCGACGCGGGCACTGTGGGTACCCGTCCTGATAACGGCATG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CAGTGGGTTAACAACATCGGCGACGCGGGCACTGTGGGTACCCGTCCTGATAACGGCATG 540

Qy        541 CTGAGCCTGGGCGTTTCCTACCGCTTCGGTCAGGAAGATGCTGCACCGGTTGTTGCTCCG 600
```

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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CTGAGCCTGGGCGTTTCCTACCGCTTCGGTCAGGAAGATGCTGCACCGGTTGTTGCTCCG 600

Qy        601 GCTCCGGCTCCGGCTCCGGAAGTGGCTACCAAGCACTTCACCCTGAAGTCTGACGTTCTG 660
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GCTCCGGCTCCGGCTCCGGAAGTGGCTACCAAGCACTTCACCCTGAAGTCTGACGTTCTG 660

Qy        661 TTCAACTTCAACAAAGCTACCCTGAAACCGGAAGGTCAGCAGGCTCTGGATCAGCTGTAC 720
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TTCAACTTCAACAAAGCTACCCTGAAACCGGAAGGTCAGCAGGCTCTGGATCAGCTGTAC 720

Qy        721 ACTCAGCTGAGCAACATGGATCCGAAAGACGGTTCCGCTGTTGTTCTGGGCTACACCGAC 780
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ACTCAGCTGAGCAACATGGATCCGAAAGACGGTTCCGCTGTTGTTCTGGGCTACACCGAC 780

Qy        781 CGCATCGGTTCCGAAGCTTACAACCAGCAGCTGTCTGAGAAACGTGCTCAGTCCGTTGTT 840
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CGCATCGGTTCCGAAGCTTACAACCAGCAGCTGTCTGAGAAACGTGCTCAGTCCGTTGTT 840

Qy        841 GACTACCTGGTTGCTAAAGGCATCCCGGCTGGCAAAATCTCCGCTCGCGGCATGGGTGAA 900
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GACTACCTGGTTGCTAAAGGCATCCCGGCTGGCAAAATCTCCGCTCGCGGCATGGGTGAA 900

Qy        901 TCCAACCCGGTTACTGGCAACACCTGTGACAACGTGAAAGCTCGCGCTGCCCTGATCGAT 960
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TCCAACCCGGTTACTGGCAACACCTGTGACAACGTGAAAGCTCGCGCTGCCCTGATCGAT 960

Qy        961 TGCCTGGCTCCGGATCGTCGTGTAGAGATCGAAGTTAAAGGCTACAAAGAAGTTGTAACT 1020
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TGCCTGGCTCCGGATCGTCGTGTAGAGATCGAAGTTAAAGGCTACAAAGAAGTTGTAACT 1020

Qy       1021 CAGCCGGCGGGTTAA 1035
                |||||||||||||||
Db       1021 CAGCCGGCGGGTTAA 1035
```

RESULT 6
AAA63956
ID AAA63956 standard; DNA; 1035 BP.
XX
AC AAA63956;
XX
DT 04-DEC-2000 (first entry)
XX
DE DNA encoding an outer membrane protein A (OmpA), designated P40.
XX
KW Outer membrane protein A; OmpA; P40; cytotoxic T cell response; tumour;
KW CTL response; tumour cell; vaccine; melanoma; genetic vaccine; ss.
XX
OS Klebsiella pneumoniae.
XX
FH Key   Location/Qualifiers
FT CDS   1. .1035
FT   /*tag= a
FT   /product= "outer membrane protein A (OmpA) P40"
XX
PN WO200048629-A1.
XX
PD 24-AUG-2000.
XX
PF 17-FEB-2000; 2000WO-FR000394.
XX
PR 17-FEB-1999; 99FR-00001917.
XX
PA (FABR) FABRE MEDICAMENT SA PIERRE.
XX
PI Renno T, Romero P, Miconnet I, Carottini J, Bonnefoy J;
XX
DR WPI; 2000-549238/50.
DR P-PSDB; AAB08341.
XX
PT Use of enterobacterial outer membrane protein A in vaccines, used to
PT treat or prevent melanoma, includes melanoma-specific peptide and induces
PT cytotoxic lymphocyte response.
XX
PS Example 1; Page 28-29; 35pp; French.
XX
CC The present sequence encodes a Klebsiella pneumoniae outer membrane
CC protein A (OmpA), designated P40. The enterobacterial OmpA polypeptide,
CC or its fragments, is used for preparing a composition that induces, or
CC increases, the cytotoxic T cell (CTL) response against tumour cells.
CC Compositions containing OmpA, optionally mixed with or coupled to a
CC suitable antigen or hapten, are used as vaccines for treatment or
CC prevention of tumors, particularly where associated with an antigen and
CC specifically melanoma. Nucleic acids that encode OmpA (or its fusion with
CC antigens or haptens) are useful as genetic vaccines again for treating
CC tumors
XX
SQ Sequence 1035 BP; 227 A; 283 C; 288 G; 237 T; 0 U; 0 Other;

```
  Query Match             100.0%;  Score 1035;  DB 3;  Length 1035;
  Best Local Similarity   100.0%;  Pred. No. 3.5e-283;
  Matches 1035;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGAAAGCAATTTTCGTACTGAATGCGGCTCCGAAAGATAACACCTGGTATGCAGGTGGT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGAAAGCAATTTTCGTACTGAATGCGGCTCCGAAAGATAACACCTGGTATGCAGGTGGT 60

Qy         61 AAACTGGGTTGGTCCCAGTATCACGACACCGGTTTCTACGGTAACGGTTTCCAGAACAAC 120
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Db         61 AAACTGGGTTGGTCCCAGTATCACGACACCGGTTTCTACGGTAACGGTTTCCAGAACAAC 120

Qy        121 AACGGTCCGACCCGTAACGATCAGCTTGGTGCTGGTGCGTTCGGTGGTTACCAGGTTAAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AACGGTCCGACCCGTAACGATCAGCTTGGTGCTGGTGCGTTCGGTGGTTACCAGGTTAAC 180

Qy        181 CCGTACCTCGGTTTCGAAATGGGTTATGACTGGCTGGGCCGTATGGCATATAAAGGCAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CCGTACCTCGGTTTCGAAATGGGTTATGACTGGCTGGGCCGTATGGCATATAAAGGCAGC 240

Qy        241 GTTGACAACGGTGCTTTCAAAGCTCAGGGCGTTCAGCTGACCGCTAAACTGGGTTACCCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GTTGACAACGGTGCTTTCAAAGCTCAGGGCGTTCAGCTGACCGCTAAACTGGGTTACCCG 300

Qy        301 ATCACTGACGATCTGGACATCTACACCCGTCTGGGCGGCATGGTTTGGCGCGCTGACTCC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ATCACTGACGATCTGGACATCTACACCCGTCTGGGCGGCATGGTTTGGCGCGCTGACTCC 360

Qy        361 AAAGGCAACTACGCTTCTACCGGCGTTTCCCGTAGCGAACACGACACTGGCGTTTCCCCA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGGCAACTACGCTTCTACCGGCGTTTCCCGTAGCGAACACGACACTGGCGTTTCCCCA 420

Qy        421 GTATTTGCTGGCGGCGTAGAGTGGGCTGTTACTCGTGACATCGCTACCCGTCTGGAATAC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GTATTTGCTGGCGGCGTAGAGTGGGCTGTTACTCGTGACATCGCTACCCGTCTGGAATAC 480

Qy        481 CAGTGGGTTAACAACATCGGCGACGCGGGCACTGTGGGTACCCGTCCTGATAACGGCATG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CAGTGGGTTAACAACATCGGCGACGCGGGCACTGTGGGTACCCGTCCTGATAACGGCATG 540

Qy        541 CTGAGCCTGGGCGTTTCCTACCGCTTCGGTCAGGAAGATGCTGCACCGGTTGTTGCTCCG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CTGAGCCTGGGCGTTTCCTACCGCTTCGGTCAGGAAGATGCTGCACCGGTTGTTGCTCCG 600

Qy        601 GCTCCGGCTCCGGCTCCGGAAGTGGCTACCAAGCACTTCACCCTGAAGTCTGACGTTCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GCTCCGGCTCCGGCTCCGGAAGTGGCTACCAAGCACTTCACCCTGAAGTCTGACGTTCTG 660

Qy        661 TTCAACTTCAACAAAGCTACCCTGAAACCGGAAGGTCAGCAGGCTCTGGATCAGCTGTAC 720
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Db        661 TTCAACTTCAACAAAGCTACCCTGAAACCGGAAGGTCAGCAGGCTCTGGATCAGCTGTAC 720

Qy        721 ACTCAGCTGAGCAACATGGATCCGAAAGACGGTTCCGCTGTTGTTCTGGGCTACACCGAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ACTCAGCTGAGCAACATGGATCCGAAAGACGGTTCCGCTGTTGTTCTGGGCTACACCGAC 780
```

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Qy        781 CGCATCGGTTCCGAAGCTTACAACCAGCAGCTGTCTGAGAAACGTGCTCAGTCCGTTGTT 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CGCATCGGTTCCGAAGCTTACAACCAGCAGCTGTCTGAGAAACGTGCTCAGTCCGTTGTT 840

Qy        841 GACTACCTGGTTGCTAAAGGCATCCCGGCTGGCAAAATCTCCGCTCGCGGCATGGGTGAA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GACTACCTGGTTGCTAAAGGCATCCCGGCTGGCAAAATCTCCGCTCGCGGCATGGGTGAA 900

Qy        901 TCCAACCCGGTTACTGGCAACACCTGTGACAACGTGAAAGCTCGCGCTGCCCTGATCGAT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TCCAACCCGGTTACTGGCAACACCTGTGACAACGTGAAAGCTCGCGCTGCCCTGATCGAT 960

Qy        961 TGCCTGGCTCCGGATCGTCGTGTAGAGATCGAAGTTAAAGGCTACAAAGAAGTTGTAACT 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TGCCTGGCTCCGGATCGTCGTGTAGAGATCGAAGTTAAAGGCTACAAAGAAGTTGTAACT 1020

Qy       1021 CAGCCGGCGGGTTAA 1035
              |||||||||||||||
Db       1021 CAGCCGGCGGGTTAA 1035
```

RESULT 7
AAH74731
ID AAH74731 standard; cDNA; 1035 BP.
XX
AC AAH74731;
XX
DT 29-OCT-2001 (first entry)
XX
DE Nucleotide sequence of an outer membrane protein A, P40.
XX
KW Outer membrane protein A; P40; antigen presenting cell; vaccine;
KW antiviral; antibacterial; anticancer; autoimmune disease; inflammation;
KW graft rejection; cardiovascular disease; immune deficiency; ss.
XX
OS Klebsiella pneumoniae.
XX

FH	Key	Location/Qualifiers
FT	CDS	1. .1035
FT		/*tag= a
FT		/product= "P40"

XX
PN FR2803302-A1.
XX
PD 06-JUL-2001.
XX
PF 04-JAN-2000; 2000FR-00000070.
XX
PR 04-JAN-2000; 2000FR-00000070.
XX
PA (FABR) FABRE MEDICAMENT SA PIERRE.
XX
PI Baussant T, Jeannin P, Delneste Y, Lawny F, Bonnefoy JY;
XX
DR WPI; 2001-427232/46.
DR P-PSDB; AAG63698.
XX
PT Preparing purified polypeptide soluble in absence of detergent, useful
PT for modulating the immune system, e.g. in vaccines, by removal of
PT detergent, denaturing and molecular sieving.
XX
PS Example 1; Page 22-24; 34pp; French.
XX
CC The present sequence encodes an outer membrane protein A (P40) of
CC Klebsiella pneumoniae. The protein is soluble in aqueous solvent in
CC absence of detergent. The specification describes a method for the
CC preparation of this polypeptide. The P40 protein binds selectively to
CC antigen-presenting cell, so provides targeting, proliferation and/or
CC expression of molecules by these cells. P40 is used, alone or as an
CC adjuvant, to produce therapeutic compositions that are soluble in absence
CC of detergent, especially when formulated with an antigen or hapten for
CC modulating the host's immune system. Especially, it is used to prepare
CC vaccines, especially antiviral, antibacterial or anticancer (e.g. against
CC human immune deficiency virus, respiratory syncytial virus, measles,
CC mumps, tuberculosis etc.), but also against fungi, parasites, autoimmune
CC diseases, graft rejection, cardiovascular disease, inflammation and
CC immune deficiency
XX
SQ Sequence 1035 BP; 227 A; 283 C; 288 G; 237 T; 0 U; 0 Other;

Query Match 100.0%; Score 1035; DB 4; Length 1035;
Best Local Similarity 100.0%; Pred. No. 3.5e-283;
Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ATGAAAGCAATTTTCGTACTGAATGCGGCTCCGAAAGATAACACCTGGTATGCAGGTGGT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGAAAGCAATTTTCGTACTGAATGCGGCTCCGAAAGATAACACCTGGTATGCAGGTGGT 60

Qy         61 AAACTGGGTTGGTCCCAGTATCACGACACCGGTTTCTACGGTAACGGTTTCCAGAACAAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AAACTGGGTTGGTCCCAGTATCACGACACCGGTTTCTACGGTAACGGTTTCCAGAACAAC 120

Qy        121 AACGGTCCGACCCGTAACGATCAGCTTGGTGCTGGTGCGTTCGGTGGTTACCAGGTTAAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AACGGTCCGACCCGTAACGATCAGCTTGGTGCTGGTGCGTTCGGTGGTTACCAGGTTAAC 180

Qy        181 CCGTACCTCGGTTTCGAAATGGGTTATGACTGGCTGGGCCGTATGGCATATAAAGGCAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CCGTACCTCGGTTTCGAAATGGGTTATGACTGGCTGGGCCGTATGGCATATAAAGGCAGC 240

Qy        241 GTTGACAACGGTGCTTTCAAAGCTCAGGGCGTTCAGCTGACCGCTAAACTGGGTTACCCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GTTGACAACGGTGCTTTCAAAGCTCAGGGCGTTCAGCTGACCGCTAAACTGGGTTACCCG 300

Qy        301 ATCACTGACGATCTGGACATCTACACCCGTCTGGGCGGCATGGTTTGGCGCGCTGACTCC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ATCACTGACGATCTGGACATCTACACCCGTCTGGGCGGCATGGTTTGGCGCGCTGACTCC 360

Qy        361 AAAGGCAACTACGCTTCTACCGGCGTTTCCCGTAGCGAACACGACACTGGCGTTTCCCCA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGGCAACTACGCTTCTACCGGCGTTTCCCGTAGCGAACACGACACTGGCGTTTCCCCA 420

Qy        421 GTATTTGCTGGCGGCGTAGAGTGGGCTGTTACTCGTGACATCGCTACCCGTCTGGAATAC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GTATTTGCTGGCGGCGTAGAGTGGGCTGTTACTCGTGACATCGCTACCCGTCTGGAATAC 480

Qy        481 CAGTGGGTTAACAACATCGGCGACGCGGGCACTGTGGGTACCCGTCCTGATAACGGCATG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CAGTGGGTTAACAACATCGGCGACGCGGGCACTGTGGGTACCCGTCCTGATAACGGCATG 540

Qy        541 CTGAGCCTGGGCGTTTCCTACCGCTTCGGTCAGGAAGATGCTGCACCGGTTGTTGCTCCG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CTGAGCCTGGGCGTTTCCTACCGCTTCGGTCAGGAAGATGCTGCACCGGTTGTTGCTCCG 600

Qy        601 GCTCCGGCTCCGGCTCCGGAAGTGGCTACCAAGCACTTCACCCTGAAGTCTGACGTTCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GCTCCGGCTCCGGCTCCGGAAGTGGCTACCAAGCACTTCACCCTGAAGTCTGACGTTCTG 660

Qy        661 TTCAACTTCAACAAAGCTACCCTGAAACCGGAAGGTCAGCAGGCTCTGGATCAGCTGTAC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TTCAACTTCAACAAAGCTACCCTGAAACCGGAAGGTCAGCAGGCTCTGGATCAGCTGTAC 720

Qy        721 ACTCAGCTGAGCAACATGGATCCGAAAGACGGTTCCGCTGTTGTTCTGGGCTACACCGAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ACTCAGCTGAGCAACATGGATCCGAAAGACGGTTCCGCTGTTGTTCTGGGCTACACCGAC 780

Qy        781 CGCATCGGTTCCGAAGCTTACAACCAGCAGCTGTCTGAGAAACGTGCTCAGTCCGTTGTT 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CGCATCGGTTCCGAAGCTTACAACCAGCAGCTGTCTGAGAAACGTGCTCAGTCCGTTGTT 840

Qy        841 GACTACCTGGTTGCTAAAGGCATCCCGGCTGGCAAAATCTCCGCTCGCGGCATGGGTGAA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GACTACCTGGTTGCTAAAGGCATCCCGGCTGGCAAAATCTCCGCTCGCGGCATGGGTGAA 900

Qy        901 TCCAACCCGGTTACTGGCAACACCTGTGACAACGTGAAAGCTCGCGCTGCCCTGATCGAT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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```
Db        901 TCCAACCCGGTTACTGGCAACACCTGTGACAACGTGAAAGCTCGCGCTGCCCTGATCGAT 960

Qy        961 TGCCTGGCTCCGGATCGTCGTGTAGAGATCGAAGTTAAAGGCTACAAAGAAGTTGTAACT 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TGCCTGGCTCCGGATCGTCGTGTAGAGATCGAAGTTAAAGGCTACAAAGAAGTTGTAACT 1020

Qy       1021 CAGCCGGCGGGTTAA 1035
              |||||||||||||||
Db       1021 CAGCCGGCGGGTTAA 1035


RESULT 8
AAF80152
ID   AAF80152 standard; DNA; 1032 BP.
XX
AC   AAF80152;
XX
DT   11-JUN-2001  (first entry)
XX
DE   Nucleotide sequence of an outer membrane protein A (OmpA) P40.
XX
KW   Outer membrane protein A; OmpA; P40; enterobacteria; nasal composition;
KW   respiratory syncytial virus; RSV; RSV infection; lung; respiratory tract;
KW   vaccine; ss.
XX
OS   Klebsiella pneumoniae.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1032
FT                   /*tag=  a
FT                   /product= "outer membrane protein A (OmpA) P40"
FT                   /note= "no termination codon"
XX
PN   WO200121203-A1.
XX
PD   29-MAR-2001.
XX
PF   22-SEP-2000; 2000WO-FR002626.
XX
PR   23-SEP-1999;   99FR-00011888.
XX
PA   (FABR ) FABRE MEDICAMENT SA PIERRE.
XX
PI   Corvaiea N,  Goestch L;
XX
DR   WPI; 2001-257929/26.
DR   P-PSDB; AAB67770.
XX
PT   Vaccine against respiratory syncytial virus, comprises enterobacterial
PT   outer membrane protein and viral immunogen, provides protective response
PT   throughout the respiratory tract.
XX
PS   Example 1; Page 27-28; 39pp; French.
XX
CC   The present sequence encodes an outer membrane protein A (OmpA),
CC   designated P40. Enterobacterium OmpA proteins, associated with an
CC   immunogenic peptide from respiratory syncytial virus (RSV), are used to
CC   prepare a nasal composition that induces a protective response, against
CC   RSV infection in the upper and lower (lung) respiratory tract. OmpA
CC   potentiates the immune response to some immunogenic peptides, eliminating
CC   the need for adjuvants. The method is useful for producing vaccines for
CC   prevention or treatment of RSV infections
XX
SQ   Sequence 1032 BP; 225 A; 283 C; 288 G; 236 T; 0 U; 0 Other;

  Query Match             99.7%;  Score 1032;  DB 4;  Length 1032;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-282;
  Matches 1032;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGAAAGCAATTTTCGTACTGAATGCGGCTCCGAAAGATAACACCTGGTATGCAGGTGGT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGAAAGCAATTTTCGTACTGAATGCGGCTCCGAAAGATAACACCTGGTATGCAGGTGGT 60

Qy         61 AAACTGGGTTGGTCCCAGTATCACGACACCGGTTTCTACGGTAACGGTTTCCAGAACAAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AAACTGGGTTGGTCCCAGTATCACGACACCGGTTTCTACGGTAACGGTTTCCAGAACAAC 120

Qy        121 AACGGTCCGACCCGTAACGATCAGCTTGGTGCTGGTGCGTTCGGTGGTTACCAGGTTAAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AACGGTCCGACCCGTAACGATCAGCTTGGTGCTGGTGCGTTCGGTGGTTACCAGGTTAAC 180

Qy        181 CCGTACCTCGGTTTCGAAATGGGTTATGACTGGCTGGGCCGTATGGCATATAAAGGCAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CCGTACCTCGGTTTCGAAATGGGTTATGACTGGCTGGGCCGTATGGCATATAAAGGCAGC 240

Qy        241 GTTGACAACGGTGCTTTCAAAGCTCAGGGCGTTCAGCTGACCGCTAAACTGGGTTACCCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GTTGACAACGGTGCTTTCAAAGCTCAGGGCGTTCAGCTGACCGCTAAACTGGGTTACCCG 300

Qy        301 ATCACTGACGATCTGGACATCTACACCCGTCTGGGCGGCATGGTTTGGCGCGCTGACTCC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ATCACTGACGATCTGGACATCTACACCCGTCTGGGCGGCATGGTTTGGCGCGCTGACTCC 360

Qy        361 AAAGGCAACTACGCTTCTACCGGCGTTTCCCGTAGCGAACACGACACTGGCGTTTCCCCA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGGCAACTACGCTTCTACCGGCGTTTCCCGTAGCGAACACGACACTGGCGTTTCCCCA 420

Qy        421 GTATTTGCTGGCGGCGTAGAGTGGGCTGTTACTCGTGACATCGCTACCCGTCTGGAATAC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GTATTTGCTGGCGGCGTAGAGTGGGCTGTTACTCGTGACATCGCTACCCGTCTGGAATAC 480

Qy        481 CAGTGGGTTAACAACATCGGCGACGCGGGCACTGTGGGTACCCGTCCTGATAACGGCATG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CAGTGGGTTAACAACATCGGCGACGCGGGCACTGTGGGTACCCGTCCTGATAACGGCATG 540

Qy        541 CTGAGCCTGGGCGTTTCCTACCGCTTCGGTCAGGAAGATGCTGCACCGGTTGTTGCTCCG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CTGAGCCTGGGCGTTTCCTACCGCTTCGGTCAGGAAGATGCTGCACCGGTTGTTGCTCCG 600

Qy        601 GCTCCGGCTCCGGCTCCGGAAGTGGCTACCAAGCACTTCACCCTGAAGTCTGACGTTCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GCTCCGGCTCCGGCTCCGGAAGTGGCTACCAAGCACTTCACCCTGAAGTCTGACGTTCTG 660

Qy        661 TTCAACTTCAACAAAGCTACCCTGAAACCGGAAGGTCAGCAGGCTCTGGATCAGCTGTAC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TTCAACTTCAACAAAGCTACCCTGAAACCGGAAGGTCAGCAGGCTCTGGATCAGCTGTAC 720

Qy        721 ACTCAGCTGAGCAACATGGATCCGAAAGACGGTTCCGCTGTTGTTCTGGGCTACACCGAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ACTCAGCTGAGCAACATGGATCCGAAAGACGGTTCCGCTGTTGTTCTGGGCTACACCGAC 780

Qy        781 CGCATCGGTTCCGAAGCTTACAACCAGCAGCTGTCTGAGAAACGTGCTCAGTCCGTTGTT 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CGCATCGGTTCCGAAGCTTACAACCAGCAGCTGTCTGAGAAACGTGCTCAGTCCGTTGTT 840

Qy        841 GACTACCTGGTTGCTAAAGGCATCCCGGCTGGCAAAATCTCCGCTCGCGGCATGGGTGAA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GACTACCTGGTTGCTAAAGGCATCCCGGCTGGCAAAATCTCCGCTCGCGGCATGGGTGAA 900

Qy        901 TCCAACCCGGTTACTGGCAACACCTGTGACAACGTGAAAGCTCGCGCTGCCCTGATCGAT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TCCAACCCGGTTACTGGCAACACCTGTGACAACGTGAAAGCTCGCGCTGCCCTGATCGAT 960

Qy        961 TGCCTGGCTCCGGATCGTCGTGTAGAGATCGAAGTTAAAGGCTACAAAGAAGTTGTAACT 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TGCCTGGCTCCGGATCGTCGTGTAGAGATCGAAGTTAAAGGCTACAAAGAAGTTGTAACT 1020

Qy       1021 CAGCCGGCGGGT 1032
              ||||||||||||
Db       1021 CAGCCGGCGGGT 1032


RESULT 9
AAV13868
ID   AAV13868 standard; DNA; 1035 BP.
XX
```

```
AC   AAV13868;
XX
DT   16-SEP-1998  (first entry)
XX
DE   Gene coding for LP40, a variant of OmpA protein P40 from K. pneumoniae.
XX
KW   Outer membrane protein; OmpA; LP40; immunocomplex; oligosaccharide;
KW   polysaccharide; vaccine; Salmonella; ss.
XX
OS   Synthetic.
OS   Klebsiella pneumoniae.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1035
FT                   /*tag=  a
FT                   /product= "LP40"
XX
PN   WO9741888-A1.
XX
PD   13-NOV-1997.
XX
PF   06-MAY-1997;   97WO-FR000800.
XX
PR   07-MAY-1996;   96FR-00005692.
XX
PA   (FABR ) FABRE MEDICAMENT SA PIERRE.
XX
PI   Binz H,  Haeuw J,  Svenson S;
XX
DR   WPI; 1997-558694/51.
DR   P-PSDB; AAR93797.
XX
PT   Immunogenic complex for use in anti-bacterial vaccine - comprises
PT   bacterial oligo; or poly:saccharide coupled to a Gram-negative bacterial
PT   outer membrane protein or a Streptococcal HSA binding protein.
XX
PS   Disclosure; Page 36-38; 63pp; French.
XX
CC   The patent discloses a new immunogenic complex which consists of (1) an
CC   oligo- or polysaccharide found naturally on bacteria, coupled to (2) a
CC   carrier protein chosen from (a) the human serum albumin binding protein
CC   of Streptococcus, (b) Gram-negative bacterial outer membrane proteins
CC   (Omp), or (c) fragments of these proteins. The immunogenic complex is
CC   useful in a vaccines to protect animals against infection by Salmonella,
CC   especially those belonging to antigenic specificity group O:9, including
CC   S. enteritidis, S. panama and S. dublin. A vaccine prepared using an
CC   oligosaccharide from S. enteritidis can be used to provide protection
CC   against septicaemia caused by S. typhi and against typhoid fever, as well
CC   as to protect humans and animals from toxic infections and zoonosis
CC   caused by Salmonella of the same serogroup. The carrier proteins enhance
CC   the immunogenicity of the oligo- or polysaccharide antigens. Inclusion of
CC   additional Salmonella capsule antigens, such as the Vi antigen, increases
CC   the vaccine's efficacy against encapsulated bacteria. The present
CC   sequence represents a gene coding for LP40, a preferred example of a
CC   carrier protein which can be used in the immunocomplex. LP40 is a variant
CC   of the P40 protein from the outer membrane protein of Klebsiella
CC   pneumoniae I-145. The gene can be used for recombinant expression of LP40
CC   in E. coli
XX
SQ   Sequence 1035 BP; 228 A; 284 C; 287 G; 236 T; 0 U; 0 Other;

  Query Match          99.5%;  Score 1030.2;  DB 2;  Length 1035;
  Best Local Similarity   99.7%;  Pred. No. 8e-282;
  Matches 1032;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 ATGAAAGCAATTTTCGTACTGAATGCGGCTCCGAAAGATAACACCTGGTATGCAGGTGGT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGAAAGCAATTTTCGTACTGAATGCGGCTCCGAAAGATAACACCTGGTATGCAGGTGGT 60

Qy         61 AAACTGGGTTGGTCCCAGTATCACGACACCGGTTTCTACGGTAACGGTTTCCAGAACAAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AAACTGGGTTGGTCCCAGTATCACGACACCGGTTTCTACGGTAACGGTTTCCAGAACAAC 120

Qy        121 AACGGTCCGACCCGTAACGATCAGCTTGGTGCTGGTGCGTTCGGTGGTTACCAGGTTAAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AACGGTCCGACCCGTAACGATCAGCTTGGTGCTGGTGCGTTCGGTGGTTACCAGGTTAAC 180

Qy        181 CCGTACCTCGGTTTCGAAATGGGTTATGACTGGCTGGGCCGTATGGCATATAAAGGCAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CCGTACCTCGGTTTCGAAATGGGTTATGACTGGCTGGGCCGTATGGCATATAAAGGCAGC 240

Qy        241 GTTGACAACGGTGCTTTCAAAGCTCAGGGCGTTCAGCTGACCGCTAAACTGGGTTACCCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GTTGACAACGGTGCTTTCAAAGCTCAGGGCGTTCAGCTGACCGCTAAACTGGGTTACCCG 300

Qy        301 ATCACTGACGATCTGGACATCTACACCCGTCTGGGCGGCATGGTTTGGCGCGCTGACTCC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ATCACTGACGATCTGGACATCTACACCCGTCTGGGCGGCATGGTTTGGCGCGCTGACTCC 360

Qy        361 AAAGGCAACTACGCTTCTACCGGCGTTTCCCGTAGCGAACACGACACTGGCGTTTCCCCA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGGCAACTACGCTTCTACCGGCGTTTCCCGTAGCGAACACGACACTGGCGTTTCCCCA 420

Qy        421 GTATTTGCTGGCGGCGTAGAGTGGGCTGTTACTCGTGACATCGCTACCCGTCTGGAATAC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GTATTTGCTGGCGGCGTAGAGTGGGCTGTTACTCGTGACATCGCTACCCGTCTGGAATAC 480

Qy        481 CAGTGGGTTAACAACATCGGCGACGCGGGCACTGTGGGTACCCGTCCTGATAACGGCATG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CAGTGGGTTAACAACATCGGCGACGCGGGCACTGTGGGTACCCGTCCTGATAACGGCATG 540

Qy        541 CTGAGCCTGGGCGTTTCCTACCGCTTCGGTCAGGAAGATGCTGCACCGGTTGTTGCTCCG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CTGAGCCTGGGCGTTTCCTACCGCTTCGGTCAGGAAGATGCTGCACCGGTTGTTGCTCCG 600

Qy        601 GCTCCGGCTCCGGCTCCGGAAGTGGCTACCAAGCACTTCACCCTGAAGTCTGACGTTCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GCTCCGGCTCCGGCTCCGGAAGTGGCTACCAAGCACTTCACCCTGAAGTCTGACGTTCTG 660

Qy        661 TTCAACTTCAACAAAGCTACCCTGAAACCGGAAGGTCAGCAGGCTCTGGATCAGCTGTAC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TTCAACTTCAACAAAGCTACCCTGAAACCGGAAGGTCAGCAGGCTCTGGATCAGCTGTAC 720

Qy        721 ACTCAGCTGAGCAACATGGATCCGAAAGACGGTTCCGCTGTTGTTCTGGGCTACACCGAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ACTCAGCTGAGCAACATGGATCCGAAAGACGGTTCCGCTGTTGTTCTGGGCTACACCGAC 780

Qy        781 CGCATCGGTTCCGAAGCTTACAACCAGCAGCTGTCTGAGAAACGTGCTCAGTCCGTTGTT 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CGCATCGGTTCCGAAGCTTACAACCAGCAGCTGTCTGAGAAACGTGCTCAGTCCGTTGTT 840

Qy        841 GACTACCTGGTTGCTAAAGGCATCCCGGCTGGCAAAATCTCCGCTCGCGGCATGGGTGAA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GACTACCTGGTTGCTAAAGGCATCCCGGCTGGCAAAATCTCCGCTCGCGGCATGGGTGAA 900

Qy        901 TCCAACCCGGTTACTGGCAACACCTGTGACAACGTGAAAGCTCGCGCTGCCCTGATCGAT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TCCAACCCGGTTACTGGCAACACCTGTGACAACGTGAAAGCTCGCGCTGCCCTGATCGAT 960

Qy        961 TGCCTGGCTCCGGATCGTCGTGTAGAGATCGAAGTTAAAGGCTACAAAGAAGTTGTAACT 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TGCCTGGCTCCGGATCGTCGTGTAGAGATCGAAGTTAAAGGCTACAAAGAAGTTGTAACT 1020

Qy       1021 CAGCCGGCGGGTTAA 1035
              |||||| ||| |||
Db       1021 CAGCCGCAGGGCTAA 1035


RESULT 10
AAF80153
ID   AAF80153 standard; DNA; 1356 BP.
XX
AC   AAF80153;
XX
DT   11-JUN-2001  (first entry)
XX
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```
DE   Nucleotide sequence of a fusion protein of P40 and RSV antigen.
XX
KW   Outer membrane protein A; OmpA; P40; enterobacteria; nasal composition;
KW   RSV; RSV infection; lung; respiratory tract; vaccine; ss.
XX
OS   Synthetic.
OS   Klebsiella pneumoniae.
OS   Respiratory syncytial virus.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1356
FT                   /*tag=  a
FT                   /product= "fusion protein of P40 and RSV antigen"
FT                   /note= "no termination codon"
XX
PN   WO200121203-A1.
XX
PD   29-MAR-2001.
XX
PF   22-SEP-2000; 2000WO-FR002626.
XX
PR   23-SEP-1999;   99FR-00011888.
XX
PA   (FABR ) FABRE MEDICAMENT SA PIERRE.
XX
PI   Corvaiea N,  Goestch L;
XX
DR   WPI; 2001-257929/26.
DR   P-PSDB; AAB67771.
XX
PT   Vaccine against respiratory syncytial virus, comprises enterobacterial
PT   outer membrane protein and viral immunogen, provides protective response
PT   throughout the respiratory tract.
XX
PS   Example 2; Page 29-31; 39pp; French.
XX
CC   The present sequence encodes a fusion protein comprising a Klebsiella
CC   pneumoniae outer membrane protein A (OmpA) designated P40 and a
CC   respiratory syncytial virus (RSV) antigen. Enterobacterium OmpA proteins,
CC   associated with an immunogenic peptide from RSV are used to prepare a
CC   nasal composition that induces a protective response, against RSV
CC   infection in the upper and lower (lung) respiratory tract. OmpA
CC   potentiates the immune response to some immunogenic peptides, eliminating
CC   the need for adjuvants. The method is useful for producing vaccines for
CC   prevention or treatment of RSV infections
XX
SQ   Sequence 1356 BP; 350 A; 397 C; 343 G; 266 T; 0 U; 0 Other;

  Query Match             99.1%;  Score 1026.2;  DB 4;  Length 1356;
  Best Local Similarity   99.7%;  Pred. No. 1.2e-280;
  Matches 1028;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 ATGAAAGCAATTTTCGTACTGAATGCGGCTCCGAAAGATAACACCTGGTATGCAGGTGGT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGAAAGCAATTTTCGTACTGAATGCGGCTCCGAAAGATAACACCTGGTATGCAGGTGGT 60

Qy         61 AAACTGGGTTGGTCCCAGTATCACGACACCGGTTTCTACGGTAACGGTTTCCAGAACAAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AAACTGGGTTGGTCCCAGTATCACGACACCGGTTTCTACGGTAACGGTTTCCAGAACAAC 120

Qy        121 AACGGTCCGACCCGTAACGATCAGCTTGGTGCTGGTGCGTTCGGTGGTTACCAGGTTAAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AACGGTCCGACCCGTAACGATCAGCTTGGTGCTGGTGCGTTCGGTGGTTACCAGGTTAAC 180

Qy        181 CCGTACCTCGGTTTCGAAATGGGTTATGACTGGCTGGGCCGTATGGCATATAAAGGCAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CCGTACCTCGGTTTCGAAATGGGTTATGACTGGCTGGGCCGTATGGCATATAAAGGCAGC 240

Qy        241 GTTGACAACGGTGCTTTCAAAGCTCAGGGCGTTCAGCTGACCGCTAAACTGGGTTACCCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GTTGACAACGGTGCTTTCAAAGCTCAGGGCGTTCAGCTGACCGCTAAACTGGGTTACCCG 300

Qy        301 ATCACTGACGATCTGGACATCTACACCCGTCTGGGCGGCATGGTTTGGCGCGCTGACTCC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ATCACTGACGATCTGGACATCTACACCCGTCTGGGCGGCATGGTTTGGCGCGCTGACTCC 360

Qy        361 AAAGGCAACTACGCTTCTACCGGCGTTTCCCGTAGCGAACACGACACTGGCGTTTCCCCA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGGCAACTACGCTTCTACCGGCGTTTCCCGTAGCGAACACGACACTGGCGTTTCCCCA 420

Qy        421 GTATTTGCTGGCGGCGTAGAGTGGGCTGTTACTCGTGACATCGCTACCCGTCTGGAATAC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GTATTTGCTGGCGGCGTAGAGTGGGCTGTTACTCGTGACATCGCTACCCGTCTGGAATAC 480

Qy        481 CAGTGGGTTAACAACATCGGCGACGCGGGCACTGTGGGTACCCGTCCTGATAACGGCATG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CAGTGGGTTAACAACATCGGCGACGCGGGCACTGTGGGTACCCGTCCTGATAACGGCATG 540

Qy        541 CTGAGCCTGGGCGTTTCCTACCGCTTCGGTCAGGAAGATGCTGCACCGGTTGTTGCTCCG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CTGAGCCTGGGCGTTTCCTACCGCTTCGGTCAGGAAGATGCTGCACCGGTTGTTGCTCCG 600

Qy        601 GCTCCGGCTCCGGCTCCGGAAGTGGCTACCAAGCACTTCACCCTGAAGTCTGACGTTCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GCTCCGGCTCCGGCTCCGGAAGTGGCTACCAAGCACTTCACCCTGAAGTCTGACGTTCTG 660

Qy        661 TTCAACTTCAACAAAGCTACCCTGAAACCGGAAGGTCAGCAGGCTCTGGATCAGCTGTAC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TTCAACTTCAACAAAGCTACCCTGAAACCGGAAGGTCAGCAGGCTCTGGATCAGCTGTAC 720

Qy        721 ACTCAGCTGAGCAACATGGATCCGAAAGACGGTTCCGCTGTTGTTCTGGGCTACACCGAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ACTCAGCTGAGCAACATGGATCCGAAAGACGGTTCCGCTGTTGTTCTGGGCTACACCGAC 780

Qy        781 CGCATCGGTTCCGAAGCTTACAACCAGCAGCTGTCTGAGAAACGTGCTCAGTCCGTTGTT 840
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db        781 CGCATCGGTTCCGAAGCTTACAACCAGCAGCTGTCTGAGAAACGTGCTCAGTCCGTCGTT 840

Qy        841 GACTACCTGGTTGCTAAAGGCATCCCGGCTGGCAAAATCTCCGCTCGCGGCATGGGTGAA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GACTACCTGGTTGCTAAAGGCATCCCGGCTGGCAAAATCTCCGCTCGCGGCATGGGTGAA 900

Qy        901 TCCAACCCGGTTACTGGCAACACCTGTGACAACGTGAAAGCTCGCGCTGCCCTGATCGAT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TCCAACCCGGTTACTGGCAACACCTGTGACAACGTGAAAGCTCGCGCTGCCCTGATCGAT 960

Qy        961 TGCCTGGCTCCGGATCGTCGTGTAGAGATCGAAGTTAAAGGCTACAAAGAAGTTGTAACT 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TGCCTGGCTCCGGATCGTCGTGTAGAGATCGAAGTTAAAGGCTACAAAGAAGTTGTAACT 1020

Qy       1021 CAGCCGGCGGG 1031
              |||||| |||
Db       1021 CAGCCGCAGGG 1031


RESULT 11
AAZ30477
ID   AAZ30477 standard; DNA; 1032 BP.
XX
AC   AAZ30477;
XX
DT   18-JAN-2000  (first entry)
XX
DE   K.pneumoniae OmpA gene.
XX
KW   Outer membrane protein; ompA; enterobacterium; Klebsiella pneumoniae;
KW   immunity; mammal; antigen; hapten; infection; human; bovine;
KW   respiratory syncytial virus; protective response; ss.
XX
OS   Klebsiella pneumoniae.
XX
PN   FR2776521-A1.
XX
PD   01-OCT-1999.
XX
PF   27-MAR-1998;   98FR-00003814.
```

```
XX
PR   27-MAR-1998;   98FR-00003814.
XX
PA   (FABR ) FABRE MEDICAMENT SA PIERRE.
XX
PI   Andreoni C,  Rauly I,  Nguyen TN,  Haeuw JF,  Baussant T;
XX
DR   WPI; 1999-583089/50.
DR   P-PSDB; AAY44077.
XX
PT   Immunogenic composition containing bacterial outer membranr protein
PT   conjugated or fused to antigen or hapten, for nasal administration, to
PT   protect against respiratory pathogens.
XX
PS   Disclosure; Page 17-18; 64pp; French.
XX
CC   The invention relates to the use of a fragment of a bacterial membrane
CC   protein, especially the outer membrane protein from an enterobacterium,
CC   e.g. the OmpA protein from Klebsiella pneumoniae, in a composition for
CC   nasal administration to improve immunity, in mammals, against an antigen
CC   or hapten. The antigen or hapten is derived from bacteria and viruses
CC   that cause respiratory infections e.g. the human or bovine respiratory
CC   syncytial virus. This sequence corresponds to the gene encoding the OmpA
CC   protein from Klebsiella. The antigens are shown in AAY44078-Y44149
CC   (AAZ30478-Z30538 for coding sequences). The use of a membrane protein,
CC   from a species other than that from which the antigen is derived, induces
CC   a protective response against the antigen, even without an adjuvant,
CC   since most adults will already be sensitized against the membrane
CC   protein, although the membrane protein-antigen product will induce an
CC   anti-membrane protein response even in subjects who are not pre-
CC   sensitized
XX
SQ   Sequence 1032 BP; 226 A; 285 C; 285 G; 236 T; 0 U; 0 Other;

  Query Match             98.9%;  Score 1024;  DB 2;  Length 1032;
  Best Local Similarity   99.5%;  Pred. No. 4.6e-280;
  Matches 1027;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 ATGAAAGCAATTTTCGTACTGAATGCGGCTCCGAAAGATAACACCTGGTATGCAGGTGGT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGAAAGCAATTTTCGTACTGAATGCGGCTCCGAAAGATAACACCTGGTATGCAGGTGGT 60

Qy         61 AAACTGGGTTGGTCCCAGTATCACGACACCGGTTTCTACGGTAACGGTTTCCAGAACAAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AAACTGGGTTGGTCCCAGTATCACGACACCGGTTTCTACGGTAACGGTTTCCAGAACAAC 120

Qy        121 AACGGTCCGACCCGTAACGATCAGCTTGGTGCTGGTGCGTTCGGTGGTTACCAGGTTAAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AACGGTCCGACCCGTAACGATCAGCTTGGTGCTGGTGCGTTCGGTGGTTACCAGGTTAAC 180

Qy        181 CCGTACCTCGGTTTCGAAATGGGTTATGACTGGCTGGGCCGTATGGCATATAAAGGCAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CCGTACCTCGGTTTCGAAATGGGTTATGACTGGCTGGGCCGTATGGCATATAAAGGCAGC 240

Qy        241 GTTGACAACGGTGCTTTCAAAGCTCAGGGCGTTCAGCTGACCGCTAAACTGGGTTACCCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GTTGACAACGGTGCTTTCAAAGCTCAGGGCGTTCAGCTGACCGCTAAACTGGGTTACCCG 300

Qy        301 ATCACTGACGATCTGGACATCTACACCCGTCTGGGCGGCATGGTTTGGCGCGCTGACTCC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ATCACTGACGATCTGGACATCTACACCCGTCTGGGCGGCATGGTTTGGCGCGCTGACTCC 360

Qy        361 AAAGGCAACTACGCTTCTACCGGCGTTTCCCGTAGCGAACACGACACTGGCGTTTCCCCA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGGCAACTACGCTTCTACCGGCGTTTCCCGTAGCGAACACGACACTGGCGTTTCCCCA 420

Qy        421 GTATTTGCTGGCGGCGTAGAGTGGGCTGTTACTCGTGACATCGCTACCCGTCTGGAATAC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GTATTTGCTGGCGGCGTAGAGTGGGCTGTTACTCGTGACATCGCTACCCGTCTGGAATAC 480

Qy        481 CAGTGGGTTAACAACATCGGCGACGCGGGCACTGTGGGTACCCGTCCTGATAACGGCATG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CAGTGGGTTAACAACATCGGCGACGCGGGCACTGTGGGTACCCGTCCTGATAACGGCATG 540

Qy        541 CTGAGCCTGGGCGTTTCCTACCGCTTCGGTCAGGAAGATGCTGCACCGGTTGTTGCTCCG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CTGAGCCTGGGCGTTTCCTACCGCTTCGGTCAGGAAGATGCTGCACCGGTTGTTGCTCCG 600

Qy        601 GCTCCGGCTCCGGCTCCGGAAGTGGCTACCAAGCACTTCACCCTGAAGTCTGACGTTCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GCTCCGGCTCCGGCTCCGGAAGTGGCTACCAAGCACTTCACCCTGAAGTCTGACGTTCTG 660

Qy        661 TTCAACTTCAACAAAGCTACCCTGAAACCGGAAGGTCAGCAGGCTCTGGATCAGCTGTAC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TTCAACTTCAACAAAGCTACCCTGAAACCGGAAGGTCAGCAGGCTCTGGATCAGCTGTAC 720

Qy        721 ACTCAGCTGAGCAACATGGATCCGAAAGACGGTTCCGCTGTTGTTCTGGGCTACACCGAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ACTCAGCTGAGCAACATGGATCCGAAAGACGGTTCCGCTGTTGTTCTGGGCTACACCGAC 780

Qy        781 CGCATCGGTTCCGAAGCTTACAACCAGCAGCTGTCTGAGAAACGTGCTCAGTCCGTTGTT 840
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db        781 CGCATCGGTTCCGAAGCTTACAACCAGCAGCTGTCTGAGAAACGTGCTCAGTCCGTCGTT 840

Qy        841 GACTACCTGGTTGCTAAAGGCATCCCGGCTGGCAAAATCTCCGCTCGCGGCATGGGTGAA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GACTACCTGGTTGCTAAAGGCATCCCGGCTGGCAAAATCTCCGCTCGCGGCATGGGTGAA 900

Qy        901 TCCAACCCGGTTACTGGCAACACCTGTGACAACGTGAAAGCTCGCGCTGCCCTGATCGAT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TCCAACCCGGTTACTGGCAACACCTGTGACAACGTGAAAGCTCGCGCTGCCCTGATCGAT 960

Qy        961 TGCCTGGCTCCGGATCGTCGTGTAGAGATCGAAGTTAAAGGCTACAAAGAAGTTGTAACT 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TGCCTGGCTCCGGATCGTCGTGTAGAGATCGAAGTTAAAGGCTACAAAGAAGTTGTAACT 1020

Qy       1021 CAGCCGGCGGGT 1032
              |||||  || |
Db       1021 CAGCCTCAGGCT 1032


RESULT 12
AAH78461
ID   AAH78461 standard; DNA; 1032 BP.
XX
AC   AAH78461;
XX
DT   10-DEC-2001  (first entry)
XX
DE   Nucleotide sequence of a Klebsiella protein.
XX
KW   zwitterionic detergent; immune response; vaccine; IgA production;
KW   IgG response; tumour; viral infection; bacterial infection;
KW   parasitic infection; ss.
XX
OS   Klebsiella pneumoniae.
XX
PN   FR2805163-A1.
XX
PD   24-AUG-2001.
XX
PF   21-FEB-2000; 2000FR-00002104.
XX
PR   21-FEB-2000; 2000FR-00002104.
XX
PA   (FABR ) FABRE MEDICAMENT SA PIERRE.
XX
PI   Goestch L,  Corvaia N,  Beck A,  Haeuw JF;
XX
DR   WPI; 2001-591759/67.
DR   P-PSDB; AAG67743.
XX
PT   Mucosally administered vaccines containing zwitterionic detergents to
PT   induce or improve immune response towards antigen or hapten, especially
PT   used in antibacterial, antiviral, antiparasitic or antitumor vaccines.
XX
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PS   Disclosure; Page 20-21; 26pp; French.
XX
CC   The present sequence encodes a Klebsiella protein. The protein is
CC   administered to test the adjuvant effect of zwitterionic detergents. The
CC   specification describes the use of zwitterionic detergents in the
CC   preparation of a mucosally administered pharmaceutical composition for
CC   inducing or improving the immune response of a mammal towards an antigen
CC   or hapten. In presence of zwitterionic detergents, vaccines are effective
CC   on mucosal (especially nasal) administration, which has the general
CC   advantages of inducing specific IgA production directly at the site of
CC   infection, stimulating a systemic IgG-type response (creating a secondary
CC   barrier against infection) and being simpler to carry out than
CC   administration by injection. The pharmaceutical composition is
CC   specifically a vaccine for the treatment or prophylaxis of tumours or
CC   viral, bacterial or parasitic infections
XX
SQ   Sequence 1032 BP; 226 A; 285 C; 285 G; 236 T; 0 U; 0 Other;

  Query Match             98.9%;  Score 1024;  DB 4;  Length 1032;
  Best Local Similarity   99.5%;  Pred. No. 4.6e-280;
  Matches 1027;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 ATGAAAGCAATTTTCGTACTGAATGCGGCTCCGAAAGATAACACCTGGTATGCAGGTGGT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGAAAGCAATTTTCGTACTGAATGCGGCTCCGAAAGATAACACCTGGTATGCAGGTGGT 60

Qy         61 AAACTGGGTTGGTCCCAGTATCACGACACCGGTTTCTACGGTAACGGTTTCCAGAACAAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AAACTGGGTTGGTCCCAGTATCACGACACCGGTTTCTACGGTAACGGTTTCCAGAACAAC 120

Qy        121 AACGGTCCGACCCGTAACGATCAGCTTGGTGCTGGTGCGTTCGGTGGTTACCAGGTTAAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AACGGTCCGACCCGTAACGATCAGCTTGGTGCTGGTGCGTTCGGTGGTTACCAGGTTAAC 180

Qy        181 CCGTACCTCGGTTTCGAAATGGGTTATGACTGGCTGGGCCGTATGGCATATAAAGGCAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CCGTACCTCGGTTTCGAAATGGGTTATGACTGGCTGGGCCGTATGGCATATAAAGGCAGC 240

Qy        241 GTTGACAACGGTGCTTTCAAAGCTCAGGGCGTTCAGCTGACCGCTAAACTGGGTTACCCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GTTGACAACGGTGCTTTCAAAGCTCAGGGCGTTCAGCTGACCGCTAAACTGGGTTACCCG 300

Qy        301 ATCACTGACGATCTGGACATCTACACCCGTCTGGGCGGCATGGTTTGGCGCGCTGACTCC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ATCACTGACGATCTGGACATCTACACCCGTCTGGGCGGCATGGTTTGGCGCGCTGACTCC 360

Qy        361 AAAGGCAACTACGCTTCTACCGGCGTTTCCCGTAGCGAACACGACACTGGCGTTTCCCCA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGGCAACTACGCTTCTACCGGCGTTTCCCGTAGCGAACACGACACTGGCGTTTCCCCA 420

Qy        421 GTATTTGCTGGCGGCGTAGAGTGGGCTGTTACTCGTGACATCGCTACCCGTCTGGAATAC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GTATTTGCTGGCGGCGTAGAGTGGGCTGTTACTCGTGACATCGCTACCCGTCTGGAATAC 480

Qy        481 CAGTGGGTTAACAACATCGGCGACGCGGGCACTGTGGGTACCCGTCCTGATAACGGCATG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CAGTGGGTTAACAACATCGGCGACGCGGGCACTGTGGGTACCCGTCCTGATAACGGCATG 540

Qy        541 CTGAGCCTGGGCGTTTCCTACCGCTTCGGTCAGGAAGATGCTGCACCGGTTGTTGCTCCG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CTGAGCCTGGGCGTTTCCTACCGCTTCGGTCAGGAAGATGCTGCACCGGTTGTTGCTCCG 600

Qy        601 GCTCCGGCTCCGGCTCCGGAAGTGGCTACCAAGCACTTCACCCTGAAGTCTGACGTTCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GCTCCGGCTCCGGCTCCGGAAGTGGCTACCAAGCACTTCACCCTGAAGTCTGACGTTCTG 660

Qy        661 TTCAACTTCAACAAAGCTACCCTGAAACCGGAAGGTCAGCAGGCTCTGGATCAGCTGTAC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TTCAACTTCAACAAAGCTACCCTGAAACCGGAAGGTCAGCAGGCTCTGGATCAGCTGTAC 720

Qy        721 ACTCAGCTGAGCAACATGGATCCGAAAGACGGTTCCGCTGTTGTTCTGGGCTACACCGAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ACTCAGCTGAGCAACATGGATCCGAAAGACGGTTCCGCTGTTGTTCTGGGCTACACCGAC 780

Qy        781 CGCATCGGTTCCGAAGCTTACAACCAGCAGCTGTCTGAGAAACGTGCTCAGTCCGTTGTT 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db        781 CGCATCGGTTCCGAAGCTTACAACCAGCAGCTGTCTGAGAAACGTGCTCAGTCCGTCGTT 840

Qy        841 GACTACCTGGTTGCTAAAGGCATCCCGGCTGGCAAAATCTCCGCTCGCGGCATGGGTGAA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GACTACCTGGTTGCTAAAGGCATCCCGGCTGGCAAAATCTCCGCTCGCGGCATGGGTGAA 900

Qy        901 TCCAACCCGGTTACTGGCAACACCTGTGACAACGTGAAAGCTCGCGCTGCCCTGATCGAT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TCCAACCCGGTTACTGGCAACACCTGTGACAACGTGAAAGCTCGCGCTGCCCTGATCGAT 960

Qy        961 TGCCTGGCTCCGGATCGTCGTGTAGAGATCGAAGTTAAAGGCTACAAAGAAGTTGTAACT 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TGCCTGGCTCCGGATCGTCGTGTAGAGATCGAAGTTAAAGGCTACAAAGAAGTTGTAACT 1020

Qy       1021 CAGCCGGCGGGT 1032
              |||||   || |
Db       1021 CAGCCTCAGGCT 1032
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RESULT 13
AAF90077
ID   AAF90077 standard; DNA; 1032 BP.
XX
AC   AAF90077;
XX
DT   06-AUG-2001  (first entry)
XX
DE   Nucleotide sequence of a recombinant outer membrane protein A (rP40).
XX
KW   Outer membrane protein A; rP40; OMP; enterobacterium; nasal vaccine;
KW   respiratory tract pathogen; ss.
XX
OS   Klebsiella pneumoniae.
XX
PN   FR2801219-A1.
XX
PD   25-MAY-2001.
XX
PF   18-SEP-2000; 2000FR-00011862.
XX
PR   27-MAR-1998;   98FR-00003814.
XX
PA   (FABR ) FABRE MEDICAMENT SA PIERRE.
XX
PI   Andreoni C,  Rauly I,  Nguyen T,  Haeuw JF,  Baussant T;
XX
DR   WPI; 2001-358083/38.
DR   P-PSDB; AAB84122.
XX
PT   Recombinant production of a protein, for particularly use as a carrier
PT   protein in nasal vaccines, comprises renaturation, after extraction, in
PT   the presence of specific detergents.
XX
PS   Example 1; Page 26-27; 48pp; French.
XX
CC   The present sequence encodes a recombinant outer membrane protein A,
CC   designated rP40. The specification describes a method for the recombinant
CC   production of a protein, or its fragments. The method comprises
CC   renaturation the protein, after extraction, in the presence of a solution
CC   containing one of the detergents Zwittergent 3-14, Zwittergent 3-12 and
CC   octylglucopyranoside, where the protein is not beta-interferon. The
CC   protein is especially the outer membrane protein (OMP) from an
CC   enterobacterium, and is useful as a carrier for delivering antigens or
CC   haptens in a nasal vaccine formulation, particularly directed against
CC   pathogens of the respiratory tract, e.g. respiratory syncytial virus
CC   (RSV), (para)influenza, hanta virus, Streptococci, Pneumococci and
CC   Meningococci, especially human or bovine RSV. Most adults show an
CC   antibody response to the Klebsiella pneumoniae P40, and this
CC   presensitisation stimulates the immune response to an antigen/hapten
CC   conjugated to the protein
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XX
SQ   Sequence 1032 BP; 226 A; 285 C; 285 G; 236 T; 0 U; 0 Other;

  Query Match             98.9%;  Score 1024;  DB 5;  Length 1032;
  Best Local Similarity   99.5%;  Pred. No. 4.6e-280;
  Matches 1027;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 ATGAAAGCAATTTTCGTACTGAATGCGGCTCCGAAAGATAACACCTGGTATGCAGGTGGT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGAAAGCAATTTTCGTACTGAATGCGGCTCCGAAAGATAACACCTGGTATGCAGGTGGT 60

Qy         61 AAACTGGGTTGGTCCCAGTATCACGACACCGGTTTCTACGGTAACGGTTTCCAGAACAAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AAACTGGGTTGGTCCCAGTATCACGACACCGGTTTCTACGGTAACGGTTTCCAGAACAAC 120

Qy        121 AACGGTCCGACCCGTAACGATCAGCTTGGTGCTGGTGCGTTCGGTGGTTACCAGGTTAAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AACGGTCCGACCCGTAACGATCAGCTTGGTGCTGGTGCGTTCGGTGGTTACCAGGTTAAC 180

Qy        181 CCGTACCTCGGTTTCGAAATGGGTTATGACTGGCTGGGCCGTATGGCATATAAAGGCAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CCGTACCTCGGTTTCGAAATGGGTTATGACTGGCTGGGCCGTATGGCATATAAAGGCAGC 240

Qy        241 GTTGACAACGGTGCTTTCAAAGCTCAGGGCGTTCAGCTGACCGCTAAACTGGGTTACCCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GTTGACAACGGTGCTTTCAAAGCTCAGGGCGTTCAGCTGACCGCTAAACTGGGTTACCCG 300

Qy        301 ATCACTGACGATCTGGACATCTACACCCGTCTGGGCGGCATGGTTTGGCGCGCTGACTCC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ATCACTGACGATCTGGACATCTACACCCGTCTGGGCGGCATGGTTTGGCGCGCTGACTCC 360

Qy        361 AAAGGCAACTACGCTTCTACCGGCGTTTCCCGTAGCGAACACGACACTGGCGTTTCCCCA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGGCAACTACGCTTCTACCGGCGTTTCCCGTAGCGAACACGACACTGGCGTTTCCCCA 420

Qy        421 GTATTTGCTGGCGGCGTAGAGTGGGCTGTTACTCGTGACATCGCTACCCGTCTGGAATAC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GTATTTGCTGGCGGCGTAGAGTGGGCTGTTACTCGTGACATCGCTACCCGTCTGGAATAC 480

Qy        481 CAGTGGGTTAACAACATCGGCGACGCGGGCACTGTGGGTACCCGTCCTGATAACGGCATG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CAGTGGGTTAACAACATCGGCGACGCGGGCACTGTGGGTACCCGTCCTGATAACGGCATG 540

Qy        541 CTGAGCCTGGGCGTTTCCTACCGCTTCGGTCAGGAAGATGCTGCACCGGTTGTTGCTCCG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CTGAGCCTGGGCGTTTCCTACCGCTTCGGTCAGGAAGATGCTGCACCGGTTGTTGCTCCG 600

Qy        601 GCTCCGGCTCCGGCTCCGGAAGTGGCTACCAAGCACTTCACCCTGAAGTCTGACGTTCTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GCTCCGGCTCCGGCTCCGGAAGTGGCTACCAAGCACTTCACCCTGAAGTCTGACGTTCTG 660

Qy        661 TTCAACTTCAACAAAGCTACCCTGAAACCGGAAGGTCAGCAGGCTCTGGATCAGCTGTAC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TTCAACTTCAACAAAGCTACCCTGAAACCGGAAGGTCAGCAGGCTCTGGATCAGCTGTAC 720

Qy        721 ACTCAGCTGAGCAACATGGATCCGAAAGACGGTTCCGCTGTTGTTCTGGGCTACACCGAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ACTCAGCTGAGCAACATGGATCCGAAAGACGGTTCCGCTGTTGTTCTGGGCTACACCGAC 780

Qy        781 CGCATCGGTTCCGAAGCTTACAACCAGCAGCTGTCTGAGAAACGTGCTCAGTCCGTTGTT 840
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db        781 CGCATCGGTTCCGAAGCTTACAACCAGCAGCTGTCTGAGAAACGTGCTCAGTCCGTCGTT 840

Qy        841 GACTACCTGGTTGCTAAAGGCATCCCGGCTGGCAAAATCTCCGCTCGCGGCATGGGTGAA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GACTACCTGGTTGCTAAAGGCATCCCGGCTGGCAAAATCTCCGCTCGCGGCATGGGTGAA 900

Qy        901 TCCAACCCGGTTACTGGCAACACCTGTGACAACGTGAAAGCTCGCGCTGCCCTGATCGAT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TCCAACCCGGTTACTGGCAACACCTGTGACAACGTGAAAGCTCGCGCTGCCCTGATCGAT 960

Qy        961 TGCCTGGCTCCGGATCGTCGTGTAGAGATCGAAGTTAAAGGCTACAAAGAAGTTGTAACT 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TGCCTGGCTCCGGATCGTCGTGTAGAGATCGAAGTTAAAGGCTACAAAGAAGTTGTAACT 1020

Qy       1021 CAGCCGGCGGGT 1032
              |||||   || |
Db       1021 CAGCCTCAGGCT 1032


RESULT 14
ACH94485
ID   ACH94485 standard; DNA; 1158 BP.
XX
AC   ACH94485;
XX
DT   29-JUL-2004  (first entry)
XX
DE   Klebsiella pneumoniae polynucleotide seqid 280.
XX
KW   Recombinant expression vector; transcription regulatory element;
KW   Klebsiella pneumoniae protein; antibacterial; Vaccine; gene; ds.
XX
OS   Klebsiella pneumoniae.
XX
PN   US6610836-B1.
XX
PD   26-AUG-2003.
XX
PF   27-JAN-2000; 2000US-00489039.
XX
PR   29-JAN-1999;   99US-0117747P.
XX
PA   (GENO-) GENOME THERAPEUTICS CORP.
XX
PI   Breton GL,  Osborne M;
XX
DR   WPI; 2003-895346/82.
DR   P-PSDB; ABO60934.
XX
PT   New nucleic acid encoding a Klebsiella pneumoniae polypeptide, useful for
PT   preparing a vaccine composition against Klebsiella pneumoniae.
XX
PS   Disclosure; SEQ ID NO 280; 932pp; English.
XX
CC   The invention describes a new isolated nucleic acid encoding a Klebsiella
CC   pneumoniae polypeptide. Also described are: a recombinant expression
CC   vector comprising the nucleic acid, operably linked to a transcription
CC   regulatory element; and a cell comprising the recombinant expression
CC   vector. The nucleic acid is useful for preparing a vaccine composition
CC   against Klebsiella pneumoniae. This sequence encodes a Klebsiella
CC   pneumoniae polypeptide of the invention
XX
SQ   Sequence 1158 BP; 259 A; 315 C; 322 G; 262 T; 0 U; 0 Other;

  Query Match             97.6%;  Score 1009.8;  DB 11;  Length 1158;
  Best Local Similarity   99.3%;  Pred. No. 5.1e-276;
  Matches 1014;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy         15 CGTACTGAATGCGGCTCCGAAAGATAACACCTGGTATGCAGGTGGTAAACTGGGTTGGTC 74
              ||||  | | || ||||||||||||||||||||||||||||||||||||||||||||
Db        138 CGTAGCGCAGGCCGCTCCGAAAGATAACACCTGGTATGCAGGTGGTAAACTGGGTTGGTC 197

Qy         75 CCAGTATCACGACACCGGTTTCTACGGTAACGGTTTCCAGAACAACAACGGTCCGACCCG 134
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        198 CCAGTATCACGACACCGGTTTCTACGGTAACGGTTTCCAGAACAACAACGGTCCGACCCG 257

Qy        135 TAACGATCAGCTTGGTGCTGGTGCGTTCGGTGGTTACCAGGTTAACCCGTACCTCGGTTT 194
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        258 TAACGATCAGCTTGGTGCTGGTGCGTTCGGTGGTTACCAGGTTAACCCGTACCTCGGTTT 317

Qy        195 CGAAATGGGTTATGACTGGCTGGGCCGTATGGCATATAAAGGCAGCGTTGACAACGGTGC 254
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        318 CGAAATGGGTTATGACTGGCTGGGCCGTATGGCATATAAAGGCAGCGTTGACAACGGTGC 377

Qy        255 TTTCAAAGCTCAGGGCGTTCAGCTGACCGCTAAACTGGGTTACCCGATCACTGACGATCT 314
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        378 TTTCAAAGCTCAGGGCGTTCAGCTGACCGCTAAACTGGGTTACCCGATCACTGACGATCT 437

Qy        315 GGACATCTACACCCGTCTGGGCGGCATGGTTTGGCGCGCTGACTCCAAAGGCAACTACGC 374
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        438 GGACATCTACACCCGTCTGGGCGGCATGGTTTGGCGCGCTGACTCCAAAGGCAACTACGC 497

Qy        375 TTCTACCGGCGTTTCCCGTAGCGAACACGACACTGGCGTTTCCCCAGTATTTGCTGGCGG 434
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        498 TTCTACCGGCGTTTCCCGTAGCGAACACGACACTGGCGTTTCCCCAGTATTTGCTGGCGG 557

Qy        435 CGTAGAGTGGGCTGTTACTCGTGACATCGCTACCCGTCTGGAATACCAGTGGGTTAACAA 494
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        558 CGTAGAGTGGGCTGTTACTCGTGACATCGCTACCCGTCTGGAATACCAGTGGGTTAACAA 617

Qy        495 CATCGGCGACGCGGGCACTGTGGGTACCCGTCCTGATAACGGCATGCTGAGCCTGGGCGT 554
              ||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db        618 CATCGGCGACGCGGGCACCGTGGGTACCCGTCCTGATAACGGCATGCTGAGCCTGGGCGT 677

Qy        555 TTCCTACCGCTTCGGTCAGGAAGATGCTGCACCGGTTGTTGCTCCGGCTCCGGCTCCGGC 614
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        678 TTCCTACCGCTTCGGTCAGGAAGATGCTGCACCGGTTGTTGCTCCGGCTCCGGCTCCGGC 737

Qy        615 TCCGGAAGTGGCTACCAAGCACTTCACCCTGAAGTCTGACGTTCTGTTCAACTTCAACAA 674
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        738 TCCGGAAGTGGCTACCAAGCACTTCACCCTGAAGTCTGACGTTCTGTTCAACTTCAACAA 797

Qy        675 AGCTACCCTGAAACCGGAAGGTCAGCAGGCTCTGGATCAGCTGTACACTCAGCTGAGCAA 734
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        798 AGCTACCCTGAAACCGGAAGGTCAGCAGGCTCTGGATCAGCTGTACACTCAGCTGAGCAA 857

Qy        735 CATGGATCCGAAAGACGGTTCCGCTGTTGTTCTGGGCTACACCGACCGCATCGGTTCCGA 794
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        858 CATGGATCCGAAAGACGGTTCCGCTGTTGTTCTGGGCTACACCGACCGCATCGGTTCCGA 917

Qy        795 AGCTTACAACCAGCAGCTGTCTGAGAAACGTGCTCAGTCCGTTGTTGACTACCTGGTTGC 854
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        918 AGCTTACAACCAGCAGCTGTCTGAGAAACGTGCTCAGTCCGTTGTTGACTACCTGGTTGC 977

Qy        855 TAAAGGCATCCCGGCTGGCAAAATCTCCGCTCGCGGCATGGGTGAATCCAACCCGGTTAC 914
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Db        978 TAAAGGCATCCCGGCTGGCAAAATCTCCGCTCGCGGCATGGGTGAATCCAACCCGGTTAC 1037

Qy        915 TGGCAACACCTGTGACAACGTGAAAGCTCGCGCTGCCCTGATCGATTGCCTGGCTCCGGA 974
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Db       1038 TGGCAACACCTGTGACAACGTGAAAGCTCGCGCTGCCCTGATCGATTGCCTGGCTCCGGA 1097

Qy        975 TCGTCGTGTAGAGATCGAAGTTAAAGGCTACAAAGAAGTTGTAACTCAGCCGGCGGGTTA 1034
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db       1098 TCGTCGTGTAGAGATCGAAGTTAAAGGCTACAAAGAAGTTGTAACTCAGCCGGCGGCTTA 1157

Qy       1035 A 1035
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Db       1158 A 1158
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RESULT 15
ACH94572/c
ID   ACH94572 standard; DNA; 1251 BP.
XX
AC   ACH94572;
XX
DT   29-JUL-2004  (first entry)
XX
DE   Klebsiella pneumoniae polynucleotide seqid 367.
XX
KW   Recombinant expression vector; transcription regulatory element;
KW   Klebsiella pneumoniae protein; antibacterial; Vaccine; gene; ds.
XX
OS   Klebsiella pneumoniae.
XX
PN   US6610836-B1.
XX
PD   26-AUG-2003.
XX
PF   27-JAN-2000; 2000US-00489039.
XX
PR   29-JAN-1999;   99US-0117747P.
XX
PA   (GENO-) GENOME THERAPEUTICS CORP.
XX
PI   Breton GL,  Osborne M;
XX
DR   WPI; 2003-895346/82.
DR   P-PSDB; ABO61021.
XX
PT   New nucleic acid encoding a Klebsiella pneumoniae polypeptide, useful for
PT   preparing a vaccine composition against Klebsiella pneumoniae.
XX
PS   Disclosure; SEQ ID NO 367; 932pp; English.
XX
CC   The invention describes a new isolated nucleic acid encoding a Klebsiella
CC   pneumoniae polypeptide. Also described are: a recombinant expression
CC   vector comprising the nucleic acid, operably linked to a transcription
CC   regulatory element; and a cell comprising the recombinant expression
CC   vector. The nucleic acid is useful for preparing a vaccine composition
CC   against Klebsiella pneumoniae. This sequence encodes a Klebsiella
CC   pneumoniae polypeptide of the invention
XX
SQ   Sequence 1251 BP; 282 A; 346 C; 348 G; 275 T; 0 U; 0 Other;

  Query Match             97.6%;  Score 1009.8;  DB 11;  Length 1251;
  Best Local Similarity   99.3%;  Pred. No. 5.3e-276;
  Matches 1014;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy         15 CGTACTGAATGCGGCTCCGAAAGATAACACCTGGTATGCAGGTGGTAAACTGGGTTGGTC 74
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Db       1165 CGTAGCGCAGGCCGCTCCGAAAGATAACACCTGGTATGCAGGTGGTAAACTGGGTTGGTC 1106

Qy         75 CCAGTATCACGACACCGGTTTCTACGGTAACGGTTTCCAGAACAACAACGGTCCGACCCG 134
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Qy        135 TAACGATCAGCTTGGTGCTGGTGCGTTCGGTGGTTACCAGGTTAACCCGTACCTCGGTTT 194
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Qy        195 CGAAATGGGTTATGACTGGCTGGGCCGTATGGCATATAAAGGCAGCGTTGACAACGGTGC 254
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Qy        255 TTTCAAAGCTCAGGGCGTTCAGCTGACCGCTAAACTGGGTTACCCGATCACTGACGATCT 314
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Db        925 TTTCAAAGCTCAGGGCGTTCAGCTGACCGCTAAACTGGGTTACCCGATCACTGACGATCT 866

Qy        315 GGACATCTACACCCGTCTGGGCGGCATGGTTTGGCGCGCTGACTCCAAAGGCAACTACGC 374
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        865 GGACATCTACACCCGTCTGGGCGGCATGGTTTGGCGCGCTGACTCCAAAGGCAACTACGC 806

Qy        375 TTCTACCGGCGTTTCCCGTAGCGAACACGACACTGGCGTTTCCCCAGTATTTGCTGGCGG 434
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        435 CGTAGAGTGGGCTGTTACTCGTGACATCGCTACCCGTCTGGAATACCAGTGGGTTAACAA 494
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        495 CATCGGCGACGCGGGCACTGTGGGTACCCGTCCTGATAACGGCATGCTGAGCCTGGGCGT 554
              ||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db        685 CATCGGCGACGCGGGCACCGTGGGTACCCGTCCTGATAACGGCATGCTGAGCCTGGGCGT 626

Qy        555 TTCCTACCGCTTCGGTCAGGAAGATGCTGCACCGGTTGTTGCTCCGGCTCCGGCTCCGGC 614
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        625 TTCCTACCGCTTCGGTCAGGAAGATGCTGCACCGGTTGTTGCTCCGGCTCCGGCTCCGGC 566

Qy        615 TCCGGAAGTGGCTACCAAGCACTTCACCCTGAAGTCTGACGTTCTGTTCAACTTCAACAA 674
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Qy        675 AGCTACCCTGAAACCGGAAGGTCAGCAGGCTCTGGATCAGCTGTACACTCAGCTGAGCAA 734
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Db        505 AGCTACCCTGAAACCGGAAGGTCAGCAGGCTCTGGATCAGCTGTACACTCAGCTGAGCAA 446

Qy        735 CATGGATCCGAAAGACGGTTCCGCTGTTGTTCTGGGCTACACCGACCGCATCGGTTCCGA 794
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Db        445 CATGGATCCGAAAGACGGTTCCGCTGTTGTTCTGGGCTACACCGACCGCATCGGTTCCGA 386

Qy        795 AGCTTACAACCAGCAGCTGTCTGAGAAACGTGCTCAGTCCGTTGTTGACTACCTGGTTGC 854
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        385 AGCTTACAACCAGCAGCTGTCTGAGAAACGTGCTCAGTCCGTTGTTGACTACCTGGTTGC 326

Qy        855 TAAAGGCATCCCGGCTGGCAAAATCTCCGCTCGCGGCATGGGTGAATCCAACCCGGTTAC 914
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Db        325 TAAAGGCATCCCGGCTGGCAAAATCTCCGCTCGCGGCATGGGTGAATCCAACCCGGTTAC 266

Qy        915 TGGCAACACCTGTGACAACGTGAAAGCTCGCGCTGCCCTGATCGATTGCCTGGCTCCGGA 974
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        265 TGGCAACACCTGTGACAACGTGAAAGCTCGCGCTGCCCTGATCGATTGCCTGGCTCCGGA 206

Qy        975 TCGTCGTGTAGAGATCGAAGTTAAAGGCTACAAAGAAGTTGTAACTCAGCCGGCGGGTTA 1034
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db        205 TCGTCGTGTAGAGATCGAAGTTAAAGGCTACAAAGAAGTTGTAACTCAGCCGGCGGCTTA 146

Qy       1035 A 1035
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Db        145 A 145
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Search completed: January 19, 2005, 14:11:58
Job time : 610 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: January 19, 2005, 10:19:08 ; Search time 4768 Seconds
(without alignments)
10265.277 Million cell updates/sec

Title: US-09-913-772-1
Perfect score: 1035
Sequence: 1 atgaaagcaatttcgtact.....taactcagccggcgggttaa 1035

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
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5: gb_ov:*
6: gb_pat:*
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8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	1035	100.0	1035	6	BD260130	BD260130 Use of an
	2	1035	100.0	1035	6	BD272054	BD272054 Bacterial
	3	1035	100.0	1035	6	BD275000	BD275000 Immunosti
	4	1035	100.0	1035	6	AX033528	AX033528 Sequence
	5	1035	100.0	1035	6	AX033532	AX033532 Sequence
	6	1035	100.0	1035	6	AX034418	AX034418 Sequence
	7	1035	100.0	1035	6	AX035661	AX035661 Sequence
	8	1035	100.0	1035	6	AX035701	AX035701 Sequence
	9	1035	100.0	1035	6	AX191406	AX191406 Sequence
	10	1032	99.7	1032	6	AX101162	AX101162 Sequence
	11	1030.2	99.5	1035	1	KPOUTMEMA	AJ000998 Klebsiell
	12	1030.2	99.5	1035	6	A67574	A67574 Sequence 3
	13	1026.2	99.1	1356	6	AX101164	AX101164 Sequence
	14	1024	98.9	1032	6	BD222264	BD222264 Use of ac
	15	1024	98.9	1032	6	AX016041	AX016041 Sequence
	16	1024	98.9	1032	6	AX230577	AX230577 Sequence
	17	1009.8	97.6	1158	6	AR383551	AR383551 Sequence
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	19	1008	97.4	1008	6	A47011	A47011 Sequence 13
	20	1008	97.4	1008	6	A67572	A67572 Sequence 1
	21	1008	97.4	1008	6	AR108918	AR108918 Sequence
	22	1008	97.4	1008	6	AR214589	AR214589 Sequence
	23	1008	97.4	1008	6	AR287914	AR287914 Sequence
	24	1008	97.4	1008	6	AR392815	AR392815 Sequence
	25	1008	97.4	1008	6	AX150311	AX150311 Sequence
	26	1007	97.3	1007	6	AR138189	AR138189 Sequence
	27	1007	97.3	1008	6	A51216	A51216 Sequence 1
	28	766.6	74.1	1361	1	EAOMPA	X00254 Enterobacte
	29	724.4	70.0	730	1	KPNOMPAA	M63355 K.pneumonia
	30	724.4	70.0	730	6	AR089252	AR089252 Sequence
	31	724.4	70.0	730	6	AR093452	AR093452 Sequence
	32	712.2	68.8	1791	1	SDOMPA	V01344 Shigella dy
	33	702.6	67.9	1697	1	AF234269	AF234269 Escherich
c	34	697.8	67.4	13832	1	D90734	D90734 Escherichia
c	35	697.8	67.4	18269	1	D90733	D90733 Escherichia
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c	37	697.8	67.4	301276	1	AE016758	AE016758 Escherich
	38	696.2	67.3	1041	1	AY305874	AY305874 Shigella
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	40	696.2	67.3	2270	6	AX191724	AX191724 Sequence
	41	696.2	67.3	2271	1	ECOMPA	V00307 E. coli omp
c	42	694.6	67.1	11641	1	AE005286	AE005286 Escherich
c	43	694.6	67.1	327773	1	AP002554	AP002554 Escherich
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c	45	685	66.2	254050	1	AL627269	AL627269 Salmonell

ALIGNMENTS

RESULT 1
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LOCUS BD260130 1035 bp DNA linear PAT 17-JUL-2003
DEFINITION Use of an enterobacterium protein OmpA for specific targeting towards antigen-presenting cells.
ACCESSION BD260130
VERSION BD260130.1 GI:33069900
KEYWORDS JP 2002529428-A/1.
SOURCE Klebsiella pneumoniae
ORGANISM Klebsiella pneumoniae
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Klebsiella.
REFERENCE 1 (bases 1 to 1035)
AUTHORS Bonnefoy,J.Y., Lecoanet,S., Aubry,J.P., Jeannin,P. and Baussant,T.
TITLE Use of an enterobacterium protein OmpA for specific targeting towards antigen-presenting cells
JOURNAL Patent: JP 2002529428-A 1 10-SEP-2002;
PIERRE FABRE MEDICAMENT
COMMENT OS Klebsiella pneumoniae
PN JP 2002529428-A/1
PD 10-SEP-2002
PF 08-NOV-1999 JP 2000580661
PR 06-NOV-1998 FR 98/14007
PI JEAN YVES BONNEFOY,SYBILLE LECOANET,JEAN PIERRE AUBRY,PASCALE
PI JEANNIN,
PI THIERRY BAUSSANT
PC A61K38/00,A61K35/76,A61K39/02,A61K39/385,A61K39/39,A61K48/00,
PC A61P9/00,
PC A61P25/00,A61P29/00,A61P31/00,A61P35/00,A61P37/02,A61P37/04,
PC A61P37/06,
PC C07K14/26,C07K19/00,C12N5/06,C12N15/09,A61K37/02,C12N15/00, PC C12N5/00
CC Use of an enterobacterium protein OmpA for specific targeting
CC towards
CC antigen-presenting cells
FH Key Location/Qualifiers
FT exon (1). .(1032)
FT intron (1033). .(1035)
FT CDS (1). .(1032).
FEATURES Location/Qualifiers
source 1. .1035
/organism="Klebsiella pneumoniae"

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ORIGIN

  Query Match           100.0%;  Score 1035;  DB 6;  Length 1035;
  Best Local Similarity  100.0%;  Pred. No. 1.1e-241;
  Matches 1035;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGAAAGCAATTTTCGTACTGAATGCGGCTCCGAAAGATAACACCTGGTATGCAGGTGGT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGAAAGCAATTTTCGTACTGAATGCGGCTCCGAAAGATAACACCTGGTATGCAGGTGGT 60

Qy         61 AAACTGGGTTGGTCCCAGTATCACGACACCGGTTTCTACGGTAACGGTTTCCAGAACAAC 120
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Db         61 AAACTGGGTTGGTCCCAGTATCACGACACCGGTTTCTACGGTAACGGTTTCCAGAACAAC 120

Qy        121 AACGGTCCGACCCGTAACGATCAGCTTGGTGCTGGTGCGTTCGGTGGTTACCAGGTTAAC 180
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Db        121 AACGGTCCGACCCGTAACGATCAGCTTGGTGCTGGTGCGTTCGGTGGTTACCAGGTTAAC 180

Qy        181 CCGTACCTCGGTTTCGAAATGGGTTATGACTGGCTGGGCCGTATGGCATATAAAGGCAGC 240
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Qy        241 GTTGACAACGGTGCTTTCAAAGCTCAGGGCGTTCAGCTGACCGCTAAACTGGGTTACCCG 300
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Db        301 ATCACTGACGATCTGGACATCTACACCCGTCTGGGCGGCATGGTTTGGCGCGCTGACTCC 360

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Db        481 CAGTGGGTTAACAACATCGGCGACGCGGGCACTGTGGGTACCCGTCCTGATAACGGCATG 540

Qy        541 CTGAGCCTGGGCGTTTCCTACCGCTTCGGTCAGGAAGATGCTGCACCGGTTGTTGCTCCG 600
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Db        541 CTGAGCCTGGGCGTTTCCTACCGCTTCGGTCAGGAAGATGCTGCACCGGTTGTTGCTCCG 600

Qy        601 GCTCCGGCTCCGGCTCCGGAAGTGGCTACCAAGCACTTCACCCTGAAGTCTGACGTTCTG 660
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Db        601 GCTCCGGCTCCGGCTCCGGAAGTGGCTACCAAGCACTTCACCCTGAAGTCTGACGTTCTG 660

Qy        661 TTCAACTTCAACAAAGCTACCCTGAAACCGGAAGGTCAGCAGGCTCTGGATCAGCTGTAC 720
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Db        661 TTCAACTTCAACAAAGCTACCCTGAAACCGGAAGGTCAGCAGGCTCTGGATCAGCTGTAC 720

Qy        721 ACTCAGCTGAGCAACATGGATCCGAAAGACGGTTCCGCTGTTGTTCTGGGCTACACCGAC 780
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Qy        781 CGCATCGGTTCCGAAGCTTACAACCAGCAGCTGTCTGAGAAACGTGCTCAGTCCGTTGTT 840
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Db        781 CGCATCGGTTCCGAAGCTTACAACCAGCAGCTGTCTGAGAAACGTGCTCAGTCCGTTGTT 840

Qy        841 GACTACCTGGTTGCTAAAGGCATCCCGGCTGGCAAAATCTCCGCTCGCGGCATGGGTGAA 900
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Qy        901 TCCAACCCGGTTACTGGCAACACCTGTGACAACGTGAAAGCTCGCGCTGCCCTGATCGAT 960
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Qy       1021 CAGCCGGCGGGTTAA 1035
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Db       1021 CAGCCGGCGGGTTAA 1035


RESULT 2
BD272054
LOCUS       BD272054               1035 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Bacterial membrane fractions with adjuvant efffect.
ACCESSION   BD272054
VERSION     BD272054.1  GI:33081822
KEYWORDS    JP 2002539169-A/1.
SOURCE      Klebsiella pneumoniae
  ORGANISM  Klebsiella pneumoniae
            Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
            Enterobacteriaceae; Klebsiella.
REFERENCE   1  (bases 1 to 1035)
  AUTHORS   Libon,C., Corvaia,N., NGguyen,T.N., Beck,A. and Bonnefoy,J.Y.
  TITLE     Bacterial membrane fractions with adjuvant efffect
  JOURNAL   Patent: JP 2002539169-A 1 19-NOV-2002;
            PIERRE FABRE MEDICAMENT
COMMENT     OS   Klebsiella pneumoniae
            PN   JP 2002539169-A/1
            PD   19-NOV-2002
            PF   15-MAR-2000 JP 2000604864
            PR   15-MAR-1999 FR     99/03153
            PI   CHRISTINE LIBON,NATHALIE CORVAIA,THIEN NGOC
            N'GUYEN,ALAIN BECK,
            PI   JEAN YVES BONNEFOY
            PC   A61K39/39,A61K9/107,A61K35/74,A61K38/00,A61K39/108,A61K39/155,
            PC   A61K47/48,
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            PC   A61P37/02,
            PC   C12N1/20//C07K19/00,(C12N1/20,C12R1:22),A61K37/02 CC
            Bacterial membrane fractions with adjuvant efffect FH   Key
               Location/Qualifiers
            FT   exon            (1). .(1032)
            FT   intron          (1033). .(1035)
            FT   CDS             (1). .(1032).
FEATURES             Location/Qualifiers
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ORIGIN

  Query Match           100.0%;  Score 1035;  DB 6;  Length 1035;
  Best Local Similarity  100.0%;  Pred. No. 1.1e-241;
  Matches 1035;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy         61 AAACTGGGTTGGTCCCAGTATCACGACACCGGTTTCTACGGTAACGGTTTCCAGAACAAC 120
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Db         61 AAACTGGGTTGGTCCCAGTATCACGACACCGGTTTCTACGGTAACGGTTTCCAGAACAAC 120

Qy        121 AACGGTCCGACCCGTAACGATCAGCTTGGTGCTGGTGCGTTCGGTGGTTACCAGGTTAAC 180
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Db        121 AACGGTCCGACCCGTAACGATCAGCTTGGTGCTGGTGCGTTCGGTGGTTACCAGGTTAAC 180

Qy        181 CCGTACCTCGGTTTCGAAATGGGTTATGACTGGCTGGGCCGTATGGCATATAAAGGCAGC 240
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Db        181 CCGTACCTCGGTTTCGAAATGGGTTATGACTGGCTGGGCCGTATGGCATATAAAGGCAGC 240

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Qy        301 ATCACTGACGATCTGGACATCTACACCCGTCTGGGCGGCATGGTTTGGCGCGCTGACTCC 360
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Db        301 ATCACTGACGATCTGGACATCTACACCCGTCTGGGCGGCATGGTTTGGCGCGCTGACTCC 360

Qy        361 AAAGGCAACTACGCTTCTACCGGCGTTTCCCGTAGCGAACACGACACTGGCGTTTCCCCA 420
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Db        361 AAAGGCAACTACGCTTCTACCGGCGTTTCCCGTAGCGAACACGACACTGGCGTTTCCCCA 420

Qy        421 GTATTTGCTGGCGGCGTAGAGTGGGCTGTTACTCGTGACATCGCTACCCGTCTGGAATAC 480
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Db        421 GTATTTGCTGGCGGCGTAGAGTGGGCTGTTACTCGTGACATCGCTACCCGTCTGGAATAC 480

Qy        481 CAGTGGGTTAACAACATCGGCGACGCGGGCACTGTGGGTACCCGTCCTGATAACGGCATG 540
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Db        481 CAGTGGGTTAACAACATCGGCGACGCGGGCACTGTGGGTACCCGTCCTGATAACGGCATG 540

Qy        541 CTGAGCCTGGGCGTTTCCTACCGCTTCGGTCAGGAAGATGCTGCACCGGTTGTTGCTCCG 600
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Db        541 CTGAGCCTGGGCGTTTCCTACCGCTTCGGTCAGGAAGATGCTGCACCGGTTGTTGCTCCG 600

Qy        601 GCTCCGGCTCCGGCTCCGGAAGTGGCTACCAAGCACTTCACCCTGAAGTCTGACGTTCTG 660
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Qy        661 TTCAACTTCAACAAAGCTACCCTGAAACCGGAAGGTCAGCAGGCTCTGGATCAGCTGTAC 720
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Db        661 TTCAACTTCAACAAAGCTACCCTGAAACCGGAAGGTCAGCAGGCTCTGGATCAGCTGTAC 720

Qy        721 ACTCAGCTGAGCAACATGGATCCGAAAGACGGTTCCGCTGTTGTTCTGGGCTACACCGAC 780
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Db        721 ACTCAGCTGAGCAACATGGATCCGAAAGACGGTTCCGCTGTTGTTCTGGGCTACACCGAC 780

Qy        781 CGCATCGGTTCCGAAGCTTACAACCAGCAGCTGTCTGAGAAACGTGCTCAGTCCGTTGTT 840
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Qy        841 GACTACCTGGTTGCTAAAGGCATCCCGGCTGGCAAAATCTCCGCTCGCGGCATGGGTGAA 900
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Qy        901 TCCAACCCGGTTACTGGCAACACCTGTGACAACGTGAAAGCTCGCGCTGCCCTGATCGAT 960
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Db        901 TCCAACCCGGTTACTGGCAACACCTGTGACAACGTGAAAGCTCGCGCTGCCCTGATCGAT 960

Qy        961 TGCCTGGCTCCGGATCGTCGTGTAGAGATCGAAGTTAAAGGCTACAAAGAAGTTGTAACT 1020
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Db        961 TGCCTGGCTCCGGATCGTCGTGTAGAGATCGAAGTTAAAGGCTACAAAGAAGTTGTAACT 1020

Qy       1021 CAGCCGGCGGGTTAA 1035
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Db       1021 CAGCCGGCGGGTTAA 1035
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RESULT 3
BD275000
LOCUS       BD275000                1035 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Immunostimulant bacterial membrane fractions in cancer treatment.
ACCESSION   BD275000
VERSION     BD275000.1  GI:33084768
KEYWORDS    JP 2002539170-A/1.
SOURCE      Klebsiella pneumoniae
  ORGANISM  Klebsiella pneumoniae
            Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
            Enterobacteriaceae; Klebsiella.
REFERENCE   1  (bases 1 to 1035)
  AUTHORS   Libon,C., Corvaia,N., Beck,A. and Vonnefoy,J.Y.
  TITLE     Immunostimulant bacterial membrane fractions in cancer treatment
  JOURNAL   Patent: JP 2002539170-A 1 19-NOV-2002;
            PIERRE FABRE MEDICAMENT
COMMENT     OS   Klebsiella pneumoniae
            PN   JP 2002539170-A/1
            PD   19-NOV-2002
            PF   15-MAR-2000 JP 2000604865
            PR   15-MAR-1999 FR     99/03154
            PI   christine libon,nathalie corvaia,allen beck,jan yves vonnefoy
            CC
            FH   Key             Location/Qualifiers
            FT   exon            (1). .(1032)
            FT   intron          (1033). .(1035)
            FT   CDS             (1). .(1032).
FEATURES             Location/Qualifiers
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ORIGIN
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Query Match 100.0%; Score 1035; DB 6; Length 1035;
Best Local Similarity 100.0%; Pred. No. 1.1e-241;
Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ATGAAAGCAATTTTCGTACTGAATGCGGCTCCGAAAGATAACACCTGGTATGCAGGTGGT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy         61 AAACTGGGTTGGTCCCAGTATCACGACACCGGTTTCTACGGTAACGGTTTCCAGAACAAC 120
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Qy        181 CCGTACCTCGGTTTCGAAATGGGTTATGACTGGCTGGGCCGTATGGCATATAAAGGCAGC 240
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Qy        421 GTATTTGCTGGCGGCGTAGAGTGGGCTGTTACTCGTGACATCGCTACCCGTCTGGAATAC 480
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Db        421 GTATTTGCTGGCGGCGTAGAGTGGGCTGTTACTCGTGACATCGCTACCCGTCTGGAATAC 480

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Db        541 CTGAGCCTGGGCGTTTCCTACCGCTTCGGTCAGGAAGATGCTGCACCGGTTGTTGCTCCG 600

Qy        601 GCTCCGGCTCCGGCTCCGGAAGTGGCTACCAAGCACTTCACCCTGAAGTCTGACGTTCTG 660
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Db        601 GCTCCGGCTCCGGCTCCGGAAGTGGCTACCAAGCACTTCACCCTGAAGTCTGACGTTCTG 660

Qy        661 TTCAACTTCAACAAAGCTACCCTGAAACCGGAAGGTCAGCAGGCTCTGGATCAGCTGTAC 720
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Qy        721 ACTCAGCTGAGCAACATGGATCCGAAAGACGGTTCCGCTGTTGTTCTGGGCTACACCGAC 780
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Db        721 ACTCAGCTGAGCAACATGGATCCGAAAGACGGTTCCGCTGTTGTTCTGGGCTACACCGAC 780

Qy        781 CGCATCGGTTCCGAAGCTTACAACCAGCAGCTGTCTGAGAAACGTGCTCAGTCCGTTGTT 840
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Qy        841 GACTACCTGGTTGCTAAAGGCATCCCGGCTGGCAAAATCTCCGCTCGCGGCATGGGTGAA 900
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Db        841 GACTACCTGGTTGCTAAAGGCATCCCGGCTGGCAAAATCTCCGCTCGCGGCATGGGTGAA 900

Qy        901 TCCAACCCGGTTACTGGCAACACCTGTGACAACGTGAAAGCTCGCGCTGCCCTGATCGAT 960
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Qy        961 TGCCTGGCTCCGGATCGTCGTGTAGAGATCGAAGTTAAAGGCTACAAAGAAGTTGTAACT 1020
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Db        961 TGCCTGGCTCCGGATCGTCGTGTAGAGATCGAAGTTAAAGGCTACAAAGAAGTTGTAACT 1020

Qy       1021 CAGCCGGCGGGTTAA 1035
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Db       1021 CAGCCGGCGGGTTAA 1035


RESULT 4
AX033528
LOCUS       AX033528               1035 bp    DNA     linear   PAT 21-SEP-2000
DEFINITION  Sequence 1 from Patent WO0048628.
ACCESSION   AX033528
VERSION     AX033528.1  GI:10280278
KEYWORDS    .
SOURCE      Klebsiella pneumoniae
  ORGANISM  Klebsiella pneumoniae
            Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
            Enterobacteriaceae; Klebsiella.
REFERENCE   1
  AUTHORS   Renno,T. and Bonnefoy,J.Y.
  TITLE     Use of an enterobacterium protein ompa associated with an antigen
            for generating an antiviral, antiparasitic or antitumoral cytotoxic
            response
  JOURNAL   Patent: WO 0048628-A 1 24-AUG-2000;
            PF MEDICAMENT (FR) ; RENNO TOUFIC (FR) ; BONNEFOY JEAN YVES (FR)
FEATURES             Location/Qualifiers
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     CDS             1. .1035
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                     VLFNFNKATLKPEGQQALDQLYTQLSNMDPKDGSAVVLGYTDRIGSEAYNQQLSEKRA
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                     YKEVVTQPAG"
ORIGIN

  Query Match           100.0%;  Score 1035;  DB 6;  Length 1035;
  Best Local Similarity  100.0%;  Pred. No. 1.1e-241;
  Matches 1035;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGAAAGCAATTTTCGTACTGAATGCGGCTCCGAAAGATAACACCTGGTATGCAGGTGGT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGAAAGCAATTTTCGTACTGAATGCGGCTCCGAAAGATAACACCTGGTATGCAGGTGGT 60

Qy         61 AAACTGGGTTGGTCCCAGTATCACGACACCGGTTTCTACGGTAACGGTTTCCAGAACAAC 120
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Db         61 AAACTGGGTTGGTCCCAGTATCACGACACCGGTTTCTACGGTAACGGTTTCCAGAACAAC 120

Qy        121 AACGGTCCGACCCGTAACGATCAGCTTGGTGCTGGTGCGTTCGGTGGTTACCAGGTTAAC 180
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Qy        181 CCGTACCTCGGTTTCGAAATGGGTTATGACTGGCTGGGCCGTATGGCATATAAAGGCAGC 240
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Qy        241 GTTGACAACGGTGCTTTCAAAGCTCAGGGCGTTCAGCTGACCGCTAAACTGGGTTACCCG 300
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Qy        361 AAAGGCAACTACGCTTCTACCGGCGTTTCCCGTAGCGAACACGACACTGGCGTTTCCCCA 420
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Db        421 GTATTTGCTGGCGGCGTAGAGTGGGCTGTTACTCGTGACATCGCTACCCGTCTGGAATAC 480

Qy        481 CAGTGGGTTAACAACATCGGCGACGCGGGCACTGTGGGTACCCGTCCTGATAACGGCATG 540
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Db        481 CAGTGGGTTAACAACATCGGCGACGCGGGCACTGTGGGTACCCGTCCTGATAACGGCATG 540

Qy        541 CTGAGCCTGGGCGTTTCCTACCGCTTCGGTCAGGAAGATGCTGCACCGGTTGTTGCTCCG 600
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Qy        601 GCTCCGGCTCCGGCTCCGGAAGTGGCTACCAAGCACTTCACCCTGAAGTCTGACGTTCTG 660
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Db        601 GCTCCGGCTCCGGCTCCGGAAGTGGCTACCAAGCACTTCACCCTGAAGTCTGACGTTCTG 660

Qy        661 TTCAACTTCAACAAAGCTACCCTGAAACCGGAAGGTCAGCAGGCTCTGGATCAGCTGTAC 720
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Qy        781 CGCATCGGTTCCGAAGCTTACAACCAGCAGCTGTCTGAGAAACGTGCTCAGTCCGTTGTT 840
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Qy        961 TGCCTGGCTCCGGATCGTCGTGTAGAGATCGAAGTTAAAGGCTACAAAGAAGTTGTAACT 1020
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Db        961 TGCCTGGCTCCGGATCGTCGTGTAGAGATCGAAGTTAAAGGCTACAAAGAAGTTGTAACT 1020

Qy       1021 CAGCCGGCGGGTTAA 1035
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Db       1021 CAGCCGGCGGGTTAA 1035


RESULT 5
AX033532
LOCUS       AX033532               1035 bp    DNA     linear   PAT 21-SEP-2000
DEFINITION  Sequence 1 from Patent WO0048629.
ACCESSION   AX033532
VERSION     AX033532.1  GI:10280280
KEYWORDS    .
SOURCE      Klebsiella pneumoniae
  ORGANISM  Klebsiella pneumoniae
            Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
            Enterobacteriaceae; Klebsiella.
REFERENCE   1
  AUTHORS   Miconnet,I., Romero,P., Carottini,J.C., Renno,T. and Bonnefoy,J.Y.
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  TITLE     Use of an ompa enterobacterium protein associated
  JOURNAL   Patent: WO 0048629-A 1 24-AUG-2000;
            MICONNET ISABELLE (CH) ; ROMERO PEDRO (CH) ; CAROTTINI JEAN CHARLES
            (CH) ; PF MEDICAMENT (FR) ; RENNO TOUFIC (FR) ; BONNEFOY JEAN YVES
            (FR)
FEATURES             Location/Qualifiers
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                     YKEVVTQPAG"
ORIGIN

  Query Match           100.0%;  Score 1035;  DB 6;  Length 1035;
  Best Local Similarity  100.0%;  Pred. No. 1.1e-241;
  Matches 1035;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGAAAGCAATTTTCGTACTGAATGCGGCTCCGAAAGATAACACCTGGTATGCAGGTGGT 60
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Qy         61 AAACTGGGTTGGTCCCAGTATCACGACACCGGTTTCTACGGTAACGGTTTCCAGAACAAC 120
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Qy        181 CCGTACCTCGGTTTCGAAATGGGTTATGACTGGCTGGGCCGTATGGCATATAAAGGCAGC 240
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Qy        241 GTTGACAACGGTGCTTTCAAAGCTCAGGGCGTTCAGCTGACCGCTAAACTGGGTTACCCG 300
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Qy        301 ATCACTGACGATCTGGACATCTACACCCGTCTGGGCGGCATGGTTTGGCGCGCTGACTCC 360
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Qy        421 GTATTTGCTGGCGGCGTAGAGTGGGCTGTTACTCGTGACATCGCTACCCGTCTGGAATAC 480
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Qy        541 CTGAGCCTGGGCGTTTCCTACCGCTTCGGTCAGGAAGATGCTGCACCGGTTGTTGCTCCG 600
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Qy        601 GCTCCGGCTCCGGCTCCGGAAGTGGCTACCAAGCACTTCACCCTGAAGTCTGACGTTCTG 660
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Db        601 GCTCCGGCTCCGGCTCCGGAAGTGGCTACCAAGCACTTCACCCTGAAGTCTGACGTTCTG 660

Qy        661 TTCAACTTCAACAAAGCTACCCTGAAACCGGAAGGTCAGCAGGCTCTGGATCAGCTGTAC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TTCAACTTCAACAAAGCTACCCTGAAACCGGAAGGTCAGCAGGCTCTGGATCAGCTGTAC 720

Qy        721 ACTCAGCTGAGCAACATGGATCCGAAAGACGGTTCCGCTGTTGTTCTGGGCTACACCGAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ACTCAGCTGAGCAACATGGATCCGAAAGACGGTTCCGCTGTTGTTCTGGGCTACACCGAC 780

Qy        781 CGCATCGGTTCCGAAGCTTACAACCAGCAGCTGTCTGAGAAACGTGCTCAGTCCGTTGTT 840
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Db        781 CGCATCGGTTCCGAAGCTTACAACCAGCAGCTGTCTGAGAAACGTGCTCAGTCCGTTGTT 840

Qy        841 GACTACCTGGTTGCTAAAGGCATCCCGGCTGGCAAAATCTCCGCTCGCGGCATGGGTGAA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GACTACCTGGTTGCTAAAGGCATCCCGGCTGGCAAAATCTCCGCTCGCGGCATGGGTGAA 900

Qy        901 TCCAACCCGGTTACTGGCAACACCTGTGACAACGTGAAAGCTCGCGCTGCCCTGATCGAT 960
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Db        901 TCCAACCCGGTTACTGGCAACACCTGTGACAACGTGAAAGCTCGCGCTGCCCTGATCGAT 960

Qy        961 TGCCTGGCTCCGGATCGTCGTGTAGAGATCGAAGTTAAAGGCTACAAAGAAGTTGTAACT 1020
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Db        961 TGCCTGGCTCCGGATCGTCGTGTAGAGATCGAAGTTAAAGGCTACAAAGAAGTTGTAACT 1020

Qy       1021 CAGCCGGCGGGTTAA 1035
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Db       1021 CAGCCGGCGGGTTAA 1035


RESULT 6
AX034418
LOCUS       AX034418               1035 bp    DNA     linear   PAT 22-SEP-2000
DEFINITION  Sequence 1 from Patent FR2789902.
ACCESSION   AX034418
VERSION     AX034418.1  GI:10303128
KEYWORDS    .
SOURCE      Klebsiella pneumoniae
  ORGANISM  Klebsiella pneumoniae
            Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
            Enterobacteriaceae; Klebsiella.
REFERENCE   1
  AUTHORS   Haeuw,J.F., Beck,A., Goetsch,L., Bonnefoy,J.Y. and Corvaia,N.
  JOURNAL   Patent: FR 2789902-A 1 25-AUG-2000;
            PF MEDICAMENT (FR)
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:573"
     CDS             1. .1035
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                     /transl_table=11
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                     QWVNNIGDAGTVGTRPDNGMLSLGVSYRFGQEDAAPVVAPAPAPAPEVATKHFTLKSD
                     VLFNFNKATLKPEGQQALDQLYTQLSNMDPKDGSAVVLGYTDRIGSEAYNQQLSEKRA
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                     YKEVVTQPAG"
ORIGIN

  Query Match           100.0%;  Score 1035;  DB 6;  Length 1035;
  Best Local Similarity  100.0%;  Pred. No. 1.1e-241;
  Matches 1035;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGAAAGCAATTTTCGTACTGAATGCGGCTCCGAAAGATAACACCTGGTATGCAGGTGGT 60
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Db          1 ATGAAAGCAATTTTCGTACTGAATGCGGCTCCGAAAGATAACACCTGGTATGCAGGTGGT 60

Qy         61 AAACTGGGTTGGTCCCAGTATCACGACACCGGTTTCTACGGTAACGGTTTCCAGAACAAC 120
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Db         61 AAACTGGGTTGGTCCCAGTATCACGACACCGGTTTCTACGGTAACGGTTTCCAGAACAAC 120

Qy        121 AACGGTCCGACCCGTAACGATCAGCTTGGTGCTGGTGCGTTCGGTGGTTACCAGGTTAAC 180

Db        121 AACGGTCCGACCCGTAACGATCAGCTTGGTGCTGGTGCGTTCGGTGGTTACCAGGTTAAC 180

Qy        181 CCGTACCTCGGTTTCGAAATGGGTTATGACTGGCTGGGCCGTATGGCATATAAAGGCAGC 240

Db        181 CCGTACCTCGGTTTCGAAATGGGTTATGACTGGCTGGGCCGTATGGCATATAAAGGCAGC 240

Qy        241 GTTGACAACGGTGCTTTCAAAGCTCAGGGCGTTCAGCTGACCGCTAAACTGGGTTACCCG 300

Db        241 GTTGACAACGGTGCTTTCAAAGCTCAGGGCGTTCAGCTGACCGCTAAACTGGGTTACCCG 300

Qy        301 ATCACTGACGATCTGGACATCTACACCCGTCTGGGCGGCATGGTTTGGCGCGCTGACTCC 360

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Qy        361 AAAGGCAACTACGCTTCTACCGGCGTTTCCCGTAGCGAACACGACACTGGCGTTTCCCCA 420

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Qy        421 GTATTTGCTGGCGGCGTAGAGTGGGCTGTTACTCGTGACATCGCTACCCGTCTGGAATAC 480

Db        421 GTATTTGCTGGCGGCGTAGAGTGGGCTGTTACTCGTGACATCGCTACCCGTCTGGAATAC 480

Qy        481 CAGTGGGTTAACAACATCGGCGACGCGGGCACTGTGGGTACCCGTCCTGATAACGGCATG 540

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Qy        601 GCTCCGGCTCCGGCTCCGGAAGTGGCTACCAAGCACTTCACCCTGAAGTCTGACGTTCTG 660

Db        601 GCTCCGGCTCCGGCTCCGGAAGTGGCTACCAAGCACTTCACCCTGAAGTCTGACGTTCTG 660

Qy        661 TTCAACTTCAACAAAGCTACCCTGAAACCGGAAGGTCAGCAGGCTCTGGATCAGCTGTAC 720

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Qy        781 CGCATCGGTTCCGAAGCTTACAACCAGCAGCTGTCTGAGAAACGTGCTCAGTCCGTTGTT 840

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Qy        841 GACTACCTGGTTGCTAAAGGCATCCCGGCTGGCAAAATCTCCGCTCGCGGCATGGGTGAA 900

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Qy        901 TCCAACCCGGTTACTGGCAACACCTGTGACAACGTGAAAGCTCGCGCTGCCCTGATCGAT 960

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Qy       1021 CAGCCGGCGGGTTAA 1035

Db       1021 CAGCCGGCGGGTTAA 1035


RESULT 7
AX035661
LOCUS       AX035661               1035 bp    DNA     linear   PAT 15-NOV-2000
DEFINITION  Sequence 1 from Patent WO0054790.
ACCESSION   AX035661
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VERSION     AX035661.1  GI:11191257
KEYWORDS    .
SOURCE      Klebsiella pneumoniae
  ORGANISM  Klebsiella pneumoniae
            Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
            Enterobacteriaceae; Klebsiella.
REFERENCE   1
  AUTHORS   Beck,A., Libon,C., Bonnefoy,J.Y. and Corvaia,N.
  TITLE     Immunostimulant bacterial membrane fractions in cancer treatment
  JOURNAL   Patent: WO 0054790-A 1 21-SEP-2000;
            PF MEDICAMENT (FR) ; BECK ALAIN (FR) ; LIBON CHRISTINE (FR) ;
            BONNEFOY JEAN YVES (FR) ; CORVAIA NATHALIE (FR)
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:573"
     CDS             1. .1035
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                     /codon_start=1
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                     /db_xref="GI:11191258"
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                     YKEVVTQPAG"
ORIGIN

  Query Match           100.0%;  Score 1035;  DB 6;  Length 1035;
  Best Local Similarity  100.0%;  Pred. No. 1.1e-241;
  Matches 1035;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGAAAGCAATTTTCGTACTGAATGCGGCTCCGAAAGATAACACCTGGTATGCAGGTGGT 60

Db          1 ATGAAAGCAATTTTCGTACTGAATGCGGCTCCGAAAGATAACACCTGGTATGCAGGTGGT 60

Qy         61 AAACTGGGTTGGTCCCAGTATCACGACACCGGTTTCTACGGTAACGGTTTCCAGAACAAC 120

Db         61 AAACTGGGTTGGTCCCAGTATCACGACACCGGTTTCTACGGTAACGGTTTCCAGAACAAC 120

Qy        121 AACGGTCCGACCCGTAACGATCAGCTTGGTGCTGGTGCGTTCGGTGGTTACCAGGTTAAC 180

Db        121 AACGGTCCGACCCGTAACGATCAGCTTGGTGCTGGTGCGTTCGGTGGTTACCAGGTTAAC 180

Qy        181 CCGTACCTCGGTTTCGAAATGGGTTATGACTGGCTGGGCCGTATGGCATATAAAGGCAGC 240

Db        181 CCGTACCTCGGTTTCGAAATGGGTTATGACTGGCTGGGCCGTATGGCATATAAAGGCAGC 240

Qy        241 GTTGACAACGGTGCTTTCAAAGCTCAGGGCGTTCAGCTGACCGCTAAACTGGGTTACCCG 300

Db        241 GTTGACAACGGTGCTTTCAAAGCTCAGGGCGTTCAGCTGACCGCTAAACTGGGTTACCCG 300

Qy        301 ATCACTGACGATCTGGACATCTACACCCGTCTGGGCGGCATGGTTTGGCGCGCTGACTCC 360

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Qy        361 AAAGGCAACTACGCTTCTACCGGCGTTTCCCGTAGCGAACACGACACTGGCGTTTCCCCA 420

Db        361 AAAGGCAACTACGCTTCTACCGGCGTTTCCCGTAGCGAACACGACACTGGCGTTTCCCCA 420

Qy        421 GTATTTGCTGGCGGCGTAGAGTGGGCTGTTACTCGTGACATCGCTACCCGTCTGGAATAC 480

Db        421 GTATTTGCTGGCGGCGTAGAGTGGGCTGTTACTCGTGACATCGCTACCCGTCTGGAATAC 480

Qy        481 CAGTGGGTTAACAACATCGGCGACGCGGGCACTGTGGGTACCCGTCCTGATAACGGCATG 540

Db        481 CAGTGGGTTAACAACATCGGCGACGCGGGCACTGTGGGTACCCGTCCTGATAACGGCATG 540

Qy        541 CTGAGCCTGGGCGTTTCCTACCGCTTCGGTCAGGAAGATGCTGCACCGGTTGTTGCTCCG 600
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Db        541 CTGAGCCTGGGCGTTTCCTACCGCTTCGGTCAGGAAGATGCTGCACCGGTTGTTGCTCCG 600

Qy        601 GCTCCGGCTCCGGCTCCGGAAGTGGCTACCAAGCACTTCACCCTGAAGTCTGACGTTCTG 660
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Qy        661 TTCAACTTCAACAAAGCTACCCTGAAACCGGAAGGTCAGCAGGCTCTGGATCAGCTGTAC 720
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Qy        721 ACTCAGCTGAGCAACATGGATCCGAAAGACGGTTCCGCTGTTGTTCTGGGCTACACCGAC 780
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Qy        781 CGCATCGGTTCCGAAGCTTACAACCAGCAGCTGTCTGAGAAACGTGCTCAGTCCGTTGTT 840
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Db        781 CGCATCGGTTCCGAAGCTTACAACCAGCAGCTGTCTGAGAAACGTGCTCAGTCCGTTGTT 840

Qy        841 GACTACCTGGTTGCTAAAGGCATCCCGGCTGGCAAAATCTCCGCTCGCGGCATGGGTGAA 900
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Db        841 GACTACCTGGTTGCTAAAGGCATCCCGGCTGGCAAAATCTCCGCTCGCGGCATGGGTGAA 900

Qy        901 TCCAACCCGGTTACTGGCAACACCTGTGACAACGTGAAAGCTCGCGCTGCCCTGATCGAT 960
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Db        901 TCCAACCCGGTTACTGGCAACACCTGTGACAACGTGAAAGCTCGCGCTGCCCTGATCGAT 960

Qy        961 TGCCTGGCTCCGGATCGTCGTGTAGAGATCGAAGTTAAAGGCTACAAAGAAGTTGTAACT 1020
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Db        961 TGCCTGGCTCCGGATCGTCGTGTAGAGATCGAAGTTAAAGGCTACAAAGAAGTTGTAACT 1020

Qy       1021 CAGCCGGCGGGTTAA 1035
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Db       1021 CAGCCGGCGGGTTAA 1035
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RESULT 8
AX035701
LOCUS       AX035701               1035 bp    DNA     linear   PAT 15-NOV-2000
DEFINITION  Sequence 1 from Patent WO0054789.
ACCESSION   AX035701
VERSION     AX035701.1  GI:11191297
KEYWORDS    .
SOURCE      Klebsiella pneumoniae
  ORGANISM  Klebsiella pneumoniae
            Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
            Enterobacteriaceae; Klebsiella.
REFERENCE   1
  AUTHORS   Beck,A., Libon,C., Bonnefoy,J.Y., Corvaia,N. and N Guyen,T.
  TITLE     Bacterial membrane fractions with adjuvant effect
  JOURNAL   Patent: WO 0054789-A 1 21-SEP-2000;
            PF MEDICAMENT (FR) ; BECK ALAIN (FR) ; LIBON CHRISTINE (FR) ;
            BONNEFOY JEAN YVES (FR) ; CORVAIA NATHALIE (FR) ; GUYEN THIEN NGOC
            N (FR)
FEATURES             Location/Qualifiers
     source          1. .1035
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     CDS             1. .1035
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                     /transl_table=11
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                     /db_xref="GI:11191298"
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ORIGIN
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  Query Match           100.0%;  Score 1035;  DB 6;  Length 1035;
  Best Local Similarity  100.0%;  Pred. No. 1.1e-241;
  Matches 1035;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGAAAGCAATTTTCGTACTGAATGCGGCTCCGAAAGATAACACCTGGTATGCAGGTGGT 60
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Db          1 ATGAAAGCAATTTTCGTACTGAATGCGGCTCCGAAAGATAACACCTGGTATGCAGGTGGT 60

Qy         61 AAACTGGGTTGGTCCCAGTATCACGACACCGGTTTCTACGGTAACGGTTTCCAGAACAAC 120
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Db         61 AAACTGGGTTGGTCCCAGTATCACGACACCGGTTTCTACGGTAACGGTTTCCAGAACAAC 120

Qy        121 AACGGTCCGACCCGTAACGATCAGCTTGGTGCTGGTGCGTTCGGTGGTTACCAGGTTAAC 180
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Db        121 AACGGTCCGACCCGTAACGATCAGCTTGGTGCTGGTGCGTTCGGTGGTTACCAGGTTAAC 180

Qy        181 CCGTACCTCGGTTTCGAAATGGGTTATGACTGGCTGGGCCGTATGGCATATAAAGGCAGC 240
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Db        181 CCGTACCTCGGTTTCGAAATGGGTTATGACTGGCTGGGCCGTATGGCATATAAAGGCAGC 240

Qy        241 GTTGACAACGGTGCTTTCAAAGCTCAGGGCGTTCAGCTGACCGCTAAACTGGGTTACCCG 300
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Db        241 GTTGACAACGGTGCTTTCAAAGCTCAGGGCGTTCAGCTGACCGCTAAACTGGGTTACCCG 300

Qy        301 ATCACTGACGATCTGGACATCTACACCCGTCTGGGCGGCATGGTTTGGCGCGCTGACTCC 360
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Db        301 ATCACTGACGATCTGGACATCTACACCCGTCTGGGCGGCATGGTTTGGCGCGCTGACTCC 360

Qy        361 AAAGGCAACTACGCTTCTACCGGCGTTTCCCGTAGCGAACACGACACTGGCGTTTCCCCA 420
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Qy        481 CAGTGGGTTAACAACATCGGCGACGCGGGCACTGTGGGTACCCGTCCTGATAACGGCATG 540
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Qy        541 CTGAGCCTGGGCGTTTCCTACCGCTTCGGTCAGGAAGATGCTGCACCGGTTGTTGCTCCG 600
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Db        541 CTGAGCCTGGGCGTTTCCTACCGCTTCGGTCAGGAAGATGCTGCACCGGTTGTTGCTCCG 600

Qy        601 GCTCCGGCTCCGGCTCCGGAAGTGGCTACCAAGCACTTCACCCTGAAGTCTGACGTTCTG 660
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Qy        661 TTCAACTTCAACAAAGCTACCCTGAAACCGGAAGGTCAGCAGGCTCTGGATCAGCTGTAC 720
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Qy        721 ACTCAGCTGAGCAACATGGATCCGAAAGACGGTTCCGCTGTTGTTCTGGGCTACACCGAC 780
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Qy        781 CGCATCGGTTCCGAAGCTTACAACCAGCAGCTGTCTGAGAAACGTGCTCAGTCCGTTGTT 840
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Db        841 GACTACCTGGTTGCTAAAGGCATCCCGGCTGGCAAAATCTCCGCTCGCGGCATGGGTGAA 900

Qy        901 TCCAACCCGGTTACTGGCAACACCTGTGACAACGTGAAAGCTCGCGCTGCCCTGATCGAT 960
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Db        901 TCCAACCCGGTTACTGGCAACACCTGTGACAACGTGAAAGCTCGCGCTGCCCTGATCGAT 960

Qy        961 TGCCTGGCTCCGGATCGTCGTGTAGAGATCGAAGTTAAAGGCTACAAAGAAGTTGTAACT 1020
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Db        961 TGCCTGGCTCCGGATCGTCGTGTAGAGATCGAAGTTAAAGGCTACAAAGAAGTTGTAACT 1020
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Qy       1021 CAGCCGGCGGGTTAA 1035
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Db       1021 CAGCCGGCGGGTTAA 1035


RESULT 9
AX191406
LOCUS       AX191406               1035 bp    DNA     linear   PAT 15-AUG-2001
DEFINITION  Sequence 1 from Patent WO0149705.
ACCESSION   AX191406
VERSION     AX191406.1  GI:15209619
KEYWORDS    .
SOURCE      Klebsiella pneumoniae
  ORGANISM  Klebsiella pneumoniae
            Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
            Enterobacteriaceae; Klebsiella.
REFERENCE   1
  AUTHORS   Baussant,T., Jeannin,P., Delneste,Y., Lawny,F. and Bonnefoy,J.Y.
  TITLE     Method for preparing a polypeptide soluble in an aqueous solvent in
            the absence of detergent
  JOURNAL   Patent: WO 0149705-A 1 12-JUL-2001;
            PIERRE FABRE MEDICAMENT (FR)
FEATURES             Location/Qualifiers
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ORIGIN

  Query Match           100.0%;  Score 1035;  DB 6;  Length 1035;
  Best Local Similarity  100.0%;  Pred. No. 1.1e-241;
  Matches 1035;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGAAAGCAATTTTCGTACTGAATGCGGCTCCGAAAGATAACACCTGGTATGCAGGTGGT 60
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Db          1 ATGAAAGCAATTTTCGTACTGAATGCGGCTCCGAAAGATAACACCTGGTATGCAGGTGGT 60

Qy         61 AAACTGGGTTGGTCCCAGTATCACGACACCGGTTTCTACGGTAACGGTTTCCAGAACAAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AAACTGGGTTGGTCCCAGTATCACGACACCGGTTTCTACGGTAACGGTTTCCAGAACAAC 120

Qy        121 AACGGTCCGACCCGTAACGATCAGCTTGGTGCTGGTGCGTTCGGTGGTTACCAGGTTAAC 180
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Db        121 AACGGTCCGACCCGTAACGATCAGCTTGGTGCTGGTGCGTTCGGTGGTTACCAGGTTAAC 180

Qy        181 CCGTACCTCGGTTTCGAAATGGGTTATGACTGGCTGGGCCGTATGGCATATAAAGGCAGC 240
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Db        181 CCGTACCTCGGTTTCGAAATGGGTTATGACTGGCTGGGCCGTATGGCATATAAAGGCAGC 240

Qy        241 GTTGACAACGGTGCTTTCAAAGCTCAGGGCGTTCAGCTGACCGCTAAACTGGGTTACCCG 300
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Db        241 GTTGACAACGGTGCTTTCAAAGCTCAGGGCGTTCAGCTGACCGCTAAACTGGGTTACCCG 300

Qy        301 ATCACTGACGATCTGGACATCTACACCCGTCTGGGCGGCATGGTTTGGCGCGCTGACTCC 360
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Db        301 ATCACTGACGATCTGGACATCTACACCCGTCTGGGCGGCATGGTTTGGCGCGCTGACTCC 360

Qy        361 AAAGGCAACTACGCTTCTACCGGCGTTTCCCGTAGCGAACACGACACTGGCGTTTCCCCA 420
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Db        361 AAAGGCAACTACGCTTCTACCGGCGTTTCCCGTAGCGAACACGACACTGGCGTTTCCCCA 420

Qy        421 GTATTTGCTGGCGGCGTAGAGTGGGCTGTTACTCGTGACATCGCTACCCGTCTGGAATAC 480
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Db        481 CAGTGGGTTAACAACATCGGCGACGCGGGCACTGTGGGTACCCGTCCTGATAACGGCATG 540

Qy        541 CTGAGCCTGGGCGTTTCCTACCGCTTCGGTCAGGAAGATGCTGCACCGGTTGTTGCTCCG 600
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Db        541 CTGAGCCTGGGCGTTTCCTACCGCTTCGGTCAGGAAGATGCTGCACCGGTTGTTGCTCCG 600

Qy        601 GCTCCGGCTCCGGCTCCGGAAGTGGCTACCAAGCACTTCACCCTGAAGTCTGACGTTCTG 660
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Db        601 GCTCCGGCTCCGGCTCCGGAAGTGGCTACCAAGCACTTCACCCTGAAGTCTGACGTTCTG 660

Qy        661 TTCAACTTCAACAAAGCTACCCTGAAACCGGAAGGTCAGCAGGCTCTGGATCAGCTGTAC 720
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Db        661 TTCAACTTCAACAAAGCTACCCTGAAACCGGAAGGTCAGCAGGCTCTGGATCAGCTGTAC 720

Qy        721 ACTCAGCTGAGCAACATGGATCCGAAAGACGGTTCCGCTGTTGTTCTGGGCTACACCGAC 780
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Db        721 ACTCAGCTGAGCAACATGGATCCGAAAGACGGTTCCGCTGTTGTTCTGGGCTACACCGAC 780

Qy        781 CGCATCGGTTCCGAAGCTTACAACCAGCAGCTGTCTGAGAAACGTGCTCAGTCCGTTGTT 840
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Db        781 CGCATCGGTTCCGAAGCTTACAACCAGCAGCTGTCTGAGAAACGTGCTCAGTCCGTTGTT 840

Qy        841 GACTACCTGGTTGCTAAAGGCATCCCGGCTGGCAAAATCTCCGCTCGCGGCATGGGTGAA 900
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Db        841 GACTACCTGGTTGCTAAAGGCATCCCGGCTGGCAAAATCTCCGCTCGCGGCATGGGTGAA 900

Qy        901 TCCAACCCGGTTACTGGCAACACCTGTGACAACGTGAAAGCTCGCGCTGCCCTGATCGAT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TCCAACCCGGTTACTGGCAACACCTGTGACAACGTGAAAGCTCGCGCTGCCCTGATCGAT 960

Qy        961 TGCCTGGCTCCGGATCGTCGTGTAGAGATCGAAGTTAAAGGCTACAAAGAAGTTGTAACT 1020
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Db        961 TGCCTGGCTCCGGATCGTCGTGTAGAGATCGAAGTTAAAGGCTACAAAGAAGTTGTAACT 1020

Qy       1021 CAGCCGGCGGGTTAA 1035
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Db       1021 CAGCCGGCGGGTTAA 1035


RESULT 10
AX101162
LOCUS       AX101162               1032 bp    DNA     linear   PAT 10-APR-2001
DEFINITION  Sequence 1 from Patent WO0121203.
ACCESSION   AX101162
VERSION     AX101162.1  GI:13619998
KEYWORDS    .
SOURCE      Klebsiella pneumoniae
  ORGANISM  Klebsiella pneumoniae
            Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
            Enterobacteriaceae; Klebsiella.
REFERENCE   1
  AUTHORS   corva A,N. and Goestch,L.
  TITLE     Use of an outer membrane protein a of an enterobacterium associated
            with a rsv immunogenic peptide for preparing vaccines for
            intranasal administration
  JOURNAL   Patent: WO 0121203-A 1 29-MAR-2001;
            PIERRE FABRE MEDICAMENT (FR)
FEATURES             Location/Qualifiers
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ORIGIN

Query Match 99.7%; Score 1032; DB 6; Length 1032;
Best Local Similarity 100.0%; Pred. No. 5.7e-241;
Matches 1032; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ATGAAAGCAATTTTCGTACTGAATGCGGCTCCGAAAGATAACACCTGGTATGCAGGTGGT 60
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Db          1 ATGAAAGCAATTTTCGTACTGAATGCGGCTCCGAAAGATAACACCTGGTATGCAGGTGGT 60

Qy         61 AAACTGGGTTGGTCCCAGTATCACGACACCGGTTTCTACGGTAACGGTTTCCAGAACAAC 120
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Qy        121 AACGGTCCGACCCGTAACGATCAGCTTGGTGCTGGTGCGTTCGGTGGTTACCAGGTTAAC 180
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Qy        181 CCGTACCTCGGTTTCGAAATGGGTTATGACTGGCTGGGCCGTATGGCATATAAAGGCAGC 240
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Qy        241 GTTGACAACGGTGCTTTCAAAGCTCAGGGCGTTCAGCTGACCGCTAAACTGGGTTACCCG 300
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Qy        541 CTGAGCCTGGGCGTTTCCTACCGCTTCGGTCAGGAAGATGCTGCACCGGTTGTTGCTCCG 600
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Qy        601 GCTCCGGCTCCGGCTCCGGAAGTGGCTACCAAGCACTTCACCCTGAAGTCTGACGTTCTG 660
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Db        601 GCTCCGGCTCCGGCTCCGGAAGTGGCTACCAAGCACTTCACCCTGAAGTCTGACGTTCTG 660

Qy        661 TTCAACTTCAACAAAGCTACCCTGAAACCGGAAGGTCAGCAGGCTCTGGATCAGCTGTAC 720
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Db        781 CGCATCGGTTCCGAAGCTTACAACCAGCAGCTGTCTGAGAAACGTGCTCAGTCCGTTGTT 840

Qy        841 GACTACCTGGTTGCTAAAGGCATCCCGGCTGGCAAAATCTCCGCTCGCGGCATGGGTGAA 900
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Db        841 GACTACCTGGTTGCTAAAGGCATCCCGGCTGGCAAAATCTCCGCTCGCGGCATGGGTGAA 900

Qy        901 TCCAACCCGGTTACTGGCAACACCTGTGACAACGTGAAAGCTCGCGCTGCCCTGATCGAT 960
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Db        901 TCCAACCCGGTTACTGGCAACACCTGTGACAACGTGAAAGCTCGCGCTGCCCTGATCGAT 960

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Qy       1021 CAGCCGGCGGGT 1032
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Db       1021 CAGCCGGCGGGT 1032
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RESULT 11
KPOUTMEMA
LOCUS KPOUTMEMA 1035 bp DNA linear BCT 08-JUN-2004
DEFINITION Klebsiella pneumoniae outer membrane protein A gene.
ACCESSION AJ000998
VERSION AJ000998.1 GI:3201544
KEYWORDS outer membrane protein A.
SOURCE Klebsiella pneumoniae
ORGANISM Klebsiella pneumoniae
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Klebsiella.
REFERENCE 1
AUTHORS Nguyen,T.N., Samuelson,P., Sterky,F., Merle-Poitte,C., Robert,A., Baussant,T., Haeuw,J.F., Uhlen,M., Binz,H. and Stahl,S.
TITLE Direct chromosomal sequencing, gene isolation and heterologous expression of the outer membrane protein A of Klebsiella pneumoniae
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1035)
AUTHORS Haeuw,J.F.
TITLE Direct Submission
JOURNAL Submitted (04-AUG-1997) Haeuw J.F., Biochemistry Department, Centre d'Immunologie Pierre Fabre, 5 Avenue Napoleon III. Saint Julien en Genevois, 74160, FRANCE
FEATURES Location/Qualifiers
source 1. .1035
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CDS 1. .1035
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ORIGIN

Query Match 99.5%; Score 1030.2; DB 1; Length 1035;
Best Local Similarity 99.7%; Pred. No. 1.6e-240;
Matches 1032; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy          1 ATGAAAGCAATTTTCGTACTGAATGCGGCTCCGAAAGATAACACCTGGTATGCAGGTGGT 60
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Db          1 ATGAAAGCAATTTTCGTACTGAATGCGGCTCCGAAAGATAACACCTGGTATGCAGGTGGT 60

Qy         61 AAACTGGGTTGGTCCCAGTATCACGACACCGGTTTCTACGGTAACGGTTTCCAGAACAAC 120
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Db         61 AAACTGGGTTGGTCCCAGTATCACGACACCGGTTTCTACGGTAACGGTTTCCAGAACAAC 120
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Qy        121 AACGGTCCGACCCGTAACGATCAGCTTGGTGCTGGTGCGTTCGGTGGTTACCAGGTTAAC 180
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Qy        901 TCCAACCCGGTTACTGGCAACACCTGTGACAACGTGAAAGCTCGCGCTGCCCTGATCGAT 960
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Qy        961 TGCCTGGCTCCGGATCGTCGTGTAGAGATCGAAGTTAAAGGCTACAAAGAAGTTGTAACT 1020
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Qy       1021 CAGCCGGCGGGTTAA 1035
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Db       1021 CAGCCGCAGGCTTAA 1035


RESULT 12
A67574
LOCUS       A67574                  1035 bp    DNA     linear   PAT 05-MAY-1999
DEFINITION  Sequence 3 from Patent WO9741888.
ACCESSION   A67574
VERSION     A67574.1  GI:4756438
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 1035)
  AUTHORS   Binz,H., Haeuw,J. and Svenson,S.
  TITLE     IMMUNOGENIC COMPLEX, USE, METHOD OF PREPARATION THEREOF AND VACCINE
            CONTAINING SAME
  JOURNAL   Patent: WO 9741888-A 3 13-NOV-1997;
            PF MEDICAMENT (FR)
COMMENT     Other publication FR 2748476 19971114.
FEATURES             Location/Qualifiers
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ORIGIN

  Query Match             99.5%;  Score 1030.2;  DB 6;  Length 1035;
  Best Local Similarity   99.7%;  Pred. No. 1.6e-240;
  Matches 1032;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 ATGAAAGCAATTTTCGTACTGAATGCGGCTCCGAAAGATAACACCTGGTATGCAGGTGGT 60
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Qy         61 AAACTGGGTTGGTCCCAGTATCACGACACCGGTTTCTACGGTAACGGTTTCCAGAACAAC 120
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Qy        421 GTATTTGCTGGCGGCGTAGAGTGGGCTGTTACTCGTGACATCGCTACCCGTCTGGAATAC 480
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Db        421 GTATTTGCTGGCGGCGTAGAGTGGGCTGTTACTCGTGACATCGCTACCCGTCTGGAATAC 480

Qy        481 CAGTGGGTTAACAACATCGGCGACGCGGGCACTGTGGGTACCCGTCCTGATAACGGCATG 540
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Db        481 CAGTGGGTTAACAACATCGGCGACGCGGGCACTGTGGGTACCCGTCCTGATAACGGCATG 540

Qy        541 CTGAGCCTGGGCGTTTCCTACCGCTTCGGTCAGGAAGATGCTGCACCGGTTGTTGCTCCG 600
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Db        541 CTGAGCCTGGGCGTTTCCTACCGCTTCGGTCAGGAAGATGCTGCACCGGTTGTTGCTCCG 600

Qy        601 GCTCCGGCTCCGGCTCCGGAAGTGGCTACCAAGCACTTCACCCTGAAGTCTGACGTTCTG 660
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Db        601 GCTCCGGCTCCGGCTCCGGAAGTGGCTACCAAGCACTTCACCCTGAAGTCTGACGTTCTG 660

Qy        661 TTCAACTTCAACAAAGCTACCCTGAAACCGGAAGGTCAGCAGGCTCTGGATCAGCTGTAC 720
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Db        661 TTCAACTTCAACAAAGCTACCCTGAAACCGGAAGGTCAGCAGGCTCTGGATCAGCTGTAC 720

Qy        721 ACTCAGCTGAGCAACATGGATCCGAAAGACGGTTCCGCTGTTGTTCTGGGCTACACCGAC 780
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Qy        781 CGCATCGGTTCCGAAGCTTACAACCAGCAGCTGTCTGAGAAACGTGCTCAGTCCGTTGTT 840
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Qy        841 GACTACCTGGTTGCTAAAGGCATCCCGGCTGGCAAAATCTCCGCTCGCGGCATGGGTGAA 900
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Db        841 GACTACCTGGTTGCTAAAGGCATCCCGGCTGGCAAAATCTCCGCTCGCGGCATGGGTGAA 900

Qy        901 TCCAACCCGGTTACTGGCAACACCTGTGACAACGTGAAAGCTCGCGCTGCCCTGATCGAT 960
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Db        901 TCCAACCCGGTTACTGGCAACACCTGTGACAACGTGAAAGCTCGCGCTGCCCTGATCGAT 960

Qy        961 TGCCTGGCTCCGGATCGTCGTGTAGAGATCGAAGTTAAAGGCTACAAAGAAGTTGTAACT 1020
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Db        961 TGCCTGGCTCCGGATCGTCGTGTAGAGATCGAAGTTAAAGGCTACAAAGAAGTTGTAACT 1020

Qy       1021 CAGCCGGCGGGTTAA 1035
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Db       1021 CAGCCGCAGGGCTAA 1035


RESULT 13
AX101164
LOCUS       AX101164               1356 bp    DNA     linear   PAT 10-APR-2001
DEFINITION  Sequence 3 from Patent WO0121203.
ACCESSION   AX101164
VERSION     AX101164.1  GI:13620000
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   corva A,N. and Goestch,L.
  TITLE     Use of an outer membrane protein a of an enterobacterium associated
            with a rsv immunogenic peptide for preparing vaccines for
            intranasal administration
  JOURNAL   Patent: WO 0121203-A 3 29-MAR-2001;
            PIERRE FABRE MEDICAMENT (FR)
FEATURES             Location/Qualifiers
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                     L'ADN DE KLEBSIELLA PNEUMONIAE (SEQ ID No. 1) ET DE L'ADN
                     DU VIRUS RESPIRATOIRE SYNCYTIAL (SEQ ID No. 8)"
     CDS             1. .>1356
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                     /db_xref="GI:13620001"
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                     VLFNFNKATLKPEGQQALDQLYTQLSNMDPKDGSAVVLGYTDRIGSEAYNQQLSEKRA
                     QSVVDYLVAKGIPAGKISARGMGESNPVTGNTCDNVKARAALIDCLAPDRRVEIEVKG
                     YKEVVTQPQGPGDPMTVKTKNTTTTQTQPSKPTTKQRQNKPPNKPNNDFHFEVFNFVP
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                     VD"
ORIGIN
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  Query Match             99.1%;  Score 1026.2;  DB 6;  Length 1356;
  Best Local Similarity   99.7%;  Pred. No. 1.4e-239;
  Matches 1028;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 ATGAAAGCAATTTTCGTACTGAATGCGGCTCCGAAAGATAACACCTGGTATGCAGGTGGT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGAAAGCAATTTTCGTACTGAATGCGGCTCCGAAAGATAACACCTGGTATGCAGGTGGT 60

Qy         61 AAACTGGGTTGGTCCCAGTATCACGACACCGGTTTCTACGGTAACGGTTTCCAGAACAAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AAACTGGGTTGGTCCCAGTATCACGACACCGGTTTCTACGGTAACGGTTTCCAGAACAAC 120

Qy        121 AACGGTCCGACCCGTAACGATCAGCTTGGTGCTGGTGCGTTCGGTGGTTACCAGGTTAAC 180
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Db        121 AACGGTCCGACCCGTAACGATCAGCTTGGTGCTGGTGCGTTCGGTGGTTACCAGGTTAAC 180

Qy        181 CCGTACCTCGGTTTCGAAATGGGTTATGACTGGCTGGGCCGTATGGCATATAAAGGCAGC 240
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Qy        241 GTTGACAACGGTGCTTTCAAAGCTCAGGGCGTTCAGCTGACCGCTAAACTGGGTTACCCG 300
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Qy        301 ATCACTGACGATCTGGACATCTACACCCGTCTGGGCGGCATGGTTTGGCGCGCTGACTCC 360
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Db        301 ATCACTGACGATCTGGACATCTACACCCGTCTGGGCGGCATGGTTTGGCGCGCTGACTCC 360

Qy        361 AAAGGCAACTACGCTTCTACCGGCGTTTCCCGTAGCGAACACGACACTGGCGTTTCCCCA 420
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Db        361 AAAGGCAACTACGCTTCTACCGGCGTTTCCCGTAGCGAACACGACACTGGCGTTTCCCCA 420

Qy        421 GTATTTGCTGGCGGCGTAGAGTGGGCTGTTACTCGTGACATCGCTACCCGTCTGGAATAC 480
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Db        421 GTATTTGCTGGCGGCGTAGAGTGGGCTGTTACTCGTGACATCGCTACCCGTCTGGAATAC 480

Qy        481 CAGTGGGTTAACAACATCGGCGACGCGGGCACTGTGGGTACCCGTCCTGATAACGGCATG 540
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Db        481 CAGTGGGTTAACAACATCGGCGACGCGGGCACTGTGGGTACCCGTCCTGATAACGGCATG 540

Qy        541 CTGAGCCTGGGCGTTTCCTACCGCTTCGGTCAGGAAGATGCTGCACCGGTTGTTGCTCCG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CTGAGCCTGGGCGTTTCCTACCGCTTCGGTCAGGAAGATGCTGCACCGGTTGTTGCTCCG 600

Qy        601 GCTCCGGCTCCGGCTCCGGAAGTGGCTACCAAGCACTTCACCCTGAAGTCTGACGTTCTG 660
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Db        601 GCTCCGGCTCCGGCTCCGGAAGTGGCTACCAAGCACTTCACCCTGAAGTCTGACGTTCTG 660

Qy        661 TTCAACTTCAACAAAGCTACCCTGAAACCGGAAGGTCAGCAGGCTCTGGATCAGCTGTAC 720
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Db        661 TTCAACTTCAACAAAGCTACCCTGAAACCGGAAGGTCAGCAGGCTCTGGATCAGCTGTAC 720

Qy        721 ACTCAGCTGAGCAACATGGATCCGAAAGACGGTTCCGCTGTTGTTCTGGGCTACACCGAC 780
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Db        721 ACTCAGCTGAGCAACATGGATCCGAAAGACGGTTCCGCTGTTGTTCTGGGCTACACCGAC 780

Qy        781 CGCATCGGTTCCGAAGCTTACAACCAGCAGCTGTCTGAGAAACGTGCTCAGTCCGTTGTT 840
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Db        781 CGCATCGGTTCCGAAGCTTACAACCAGCAGCTGTCTGAGAAACGTGCTCAGTCCGTCGTT 840

Qy        841 GACTACCTGGTTGCTAAAGGCATCCCGGCTGGCAAAATCTCCGCTCGCGGCATGGGTGAA 900
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Db        841 GACTACCTGGTTGCTAAAGGCATCCCGGCTGGCAAAATCTCCGCTCGCGGCATGGGTGAA 900

Qy        901 TCCAACCCGGTTACTGGCAACACCTGTGACAACGTGAAAGCTCGCGCTGCCCTGATCGAT 960
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Db        901 TCCAACCCGGTTACTGGCAACACCTGTGACAACGTGAAAGCTCGCGCTGCCCTGATCGAT 960

Qy        961 TGCCTGGCTCCGGATCGTCGTGTAGAGATCGAAGTTAAAGGCTACAAAGAAGTTGTAACT 1020
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Db        961 TGCCTGGCTCCGGATCGTCGTGTAGAGATCGAAGTTAAAGGCTACAAAGAAGTTGTAACT 1020
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Qy       1021 CAGCCGGCGGG 1031
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Db       1021 CAGCCGCAGGG 1031


RESULT 14
BD222264
LOCUS       BD222264               1032 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Use of active P40 conjugates for nasal delivery.
ACCESSION   BD222264
VERSION     BD222264.1  GI:33032034
KEYWORDS    JP 2002509897-A/1.
SOURCE      Klebsiella pneumoniae
  ORGANISM  Klebsiella pneumoniae
            Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
            Enterobacteriaceae; Klebsiella.
REFERENCE   1  (bases 1 to 1032)
  AUTHORS   Andreoni,C., Rauly,I., NGguyen,T., Haeuw,J.F. and Baussant,T.
  TITLE     Use of active P40 conjugates for nasal delivery
  JOURNAL   Patent: JP 2002509897-A 1 02-APR-2002;
            PIERRE FABRE MEDICAMENT
COMMENT     OS   Klebsiella pneumoniae
            PN   JP 2002509897-A/1
            PD   02-APR-2002
            PF   26-MAR-1999 JP 2000540854
            PR   27-MAR-1998 FR     98/03814
            PI   CHRISTINE ANDREONI,ISABELLE RAULY,THIEN N'GUYEN,JEAN FRANCOIS
            PI   HAEUW,
            PI   THIERRY BAUSSANT
            PC   A61K39/39,A61K9/00,A61K38/00,A61K39/09,A61K39/095,A61K39/12,
            PC   A61K39/145,
            PC
            A61K39/155,A61K39/385,A61K47/48,A61P37/04//C07K14/26,C07K19/00, PC
             C12N15/09,
            PC   A61K37/02,C12N15/00
            CC   rP40
            FH   Key             Location/Qualifiers
            FT   CDS             (1). .(1032).
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ORIGIN

  Query Match             98.9%;  Score 1024;  DB 6;  Length 1032;
  Best Local Similarity   99.5%;  Pred. No. 5.1e-239;
  Matches 1027;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 ATGAAAGCAATTTTCGTACTGAATGCGGCTCCGAAAGATAACACCTGGTATGCAGGTGGT 60
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Qy         61 AAACTGGGTTGGTCCCAGTATCACGACACCGGTTTCTACGGTAACGGTTTCCAGAACAAC 120
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Qy        301 ATCACTGACGATCTGGACATCTACACCCGTCTGGGCGGCATGGTTTGGCGCGCTGACTCC 360
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Db        301 ATCACTGACGATCTGGACATCTACACCCGTCTGGGCGGCATGGTTTGGCGCGCTGACTCC 360

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Db        361 AAAGGCAACTACGCTTCTACCGGCGTTTCCCGTAGCGAACACGACACTGGCGTTTCCCCA 420

Qy        421 GTATTTGCTGGCGGCGTAGAGTGGGCTGTTACTCGTGACATCGCTACCCGTCTGGAATAC 480
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Qy        541 CTGAGCCTGGGCGTTTCCTACCGCTTCGGTCAGGAAGATGCTGCACCGGTTGTTGCTCCG 600
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Db        541 CTGAGCCTGGGCGTTTCCTACCGCTTCGGTCAGGAAGATGCTGCACCGGTTGTTGCTCCG 600

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Qy        661 TTCAACTTCAACAAAGCTACCCTGAAACCGGAAGGTCAGCAGGCTCTGGATCAGCTGTAC 720
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Qy        721 ACTCAGCTGAGCAACATGGATCCGAAAGACGGTTCCGCTGTTGTTCTGGGCTACACCGAC 780
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Qy        781 CGCATCGGTTCCGAAGCTTACAACCAGCAGCTGTCTGAGAAACGTGCTCAGTCCGTTGTT 840
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Db        781 CGCATCGGTTCCGAAGCTTACAACCAGCAGCTGTCTGAGAAACGTGCTCAGTCCGTCGTT 840

Qy        841 GACTACCTGGTTGCTAAAGGCATCCCGGCTGGCAAAATCTCCGCTCGCGGCATGGGTGAA 900
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Qy        901 TCCAACCCGGTTACTGGCAACACCTGTGACAACGTGAAAGCTCGCGCTGCCCTGATCGAT 960
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Qy       1021 CAGCCGGCGGGT 1032
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Db       1021 CAGCCTCAGGCT 1032


RESULT 15
AX016041
LOCUS       AX016041               1032 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 1 from Patent WO9949892.
ACCESSION   AX016041
VERSION     AX016041.1  GI:10041662
KEYWORDS    .
SOURCE      Klebsiella pneumoniae
  ORGANISM  Klebsiella pneumoniae
            Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
            Enterobacteriaceae; Klebsiella.
REFERENCE   1
  AUTHORS   Haeuw,J.F., N'Guyen,T., Rauly,I., Andreoni,C. and Baussant,T.
  TITLE     Use of active p40 conjugates for nasal delivery
  JOURNAL   Patent: WO 9949892-A 1 07-OCT-1999;
            HAEUW JEAN FRANCOIS (FR); GUYEN THIEN N (FR); PF MEDICAMENT (FR);
            RAULY ISABELLE (FR); ANDREONI CHRISTINE (FR); BAUSSANT THIERRY (FR)
FEATURES             Location/Qualifiers
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     CDS             1. .>1032
                     /note="unnamed protein product; rP40"
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                     YKEVVTQPQA"
ORIGIN

  Query Match             98.9%;  Score 1024;  DB 6;  Length 1032;
  Best Local Similarity   99.5%;  Pred. No. 5.1e-239;
  Matches 1027;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 ATGAAAGCAATTTTCGTACTGAATGCGGCTCCGAAAGATAACACCTGGTATGCAGGTGGT 60
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Qy         61 AAACTGGGTTGGTCCCAGTATCACGACACCGGTTTCTACGGTAACGGTTTCCAGAACAAC 120
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Qy        121 AACGGTCCGACCCGTAACGATCAGCTTGGTGCTGGTGCGTTCGGTGGTTACCAGGTTAAC 180
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Qy        181 CCGTACCTCGGTTTCGAAATGGGTTATGACTGGCTGGGCCGTATGGCATATAAAGGCAGC 240
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Qy        241 GTTGACAACGGTGCTTTCAAAGCTCAGGGCGTTCAGCTGACCGCTAAACTGGGTTACCCG 300
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Qy        301 ATCACTGACGATCTGGACATCTACACCCGTCTGGGCGGCATGGTTTGGCGCGCTGACTCC 360
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Qy        481 CAGTGGGTTAACAACATCGGCGACGCGGGCACTGTGGGTACCCGTCCTGATAACGGCATG 540
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Qy        601 GCTCCGGCTCCGGCTCCGGAAGTGGCTACCAAGCACTTCACCCTGAAGTCTGACGTTCTG 660
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Db        601 GCTCCGGCTCCGGCTCCGGAAGTGGCTACCAAGCACTTCACCCTGAAGTCTGACGTTCTG 660

Qy        661 TTCAACTTCAACAAAGCTACCCTGAAACCGGAAGGTCAGCAGGCTCTGGATCAGCTGTAC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TTCAACTTCAACAAAGCTACCCTGAAACCGGAAGGTCAGCAGGCTCTGGATCAGCTGTAC 720

Qy        721 ACTCAGCTGAGCAACATGGATCCGAAAGACGGTTCCGCTGTTGTTCTGGGCTACACCGAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ACTCAGCTGAGCAACATGGATCCGAAAGACGGTTCCGCTGTTGTTCTGGGCTACACCGAC 780

Qy        781 CGCATCGGTTCCGAAGCTTACAACCAGCAGCTGTCTGAGAAACGTGCTCAGTCCGTTGTT 840
              |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db        781 CGCATCGGTTCCGAAGCTTACAACCAGCAGCTGTCTGAGAAACGTGCTCAGTCCGTCGTT 840

Qy        841 GACTACCTGGTTGCTAAAGGCATCCCGGCTGGCAAAATCTCCGCTCGCGGCATGGGTGAA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GACTACCTGGTTGCTAAAGGCATCCCGGCTGGCAAAATCTCCGCTCGCGGCATGGGTGAA 900

Qy        901 TCCAACCCGGTTACTGGCAACACCTGTGACAACGTGAAAGCTCGCGCTGCCCTGATCGAT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TCCAACCCGGTTACTGGCAACACCTGTGACAACGTGAAAGCTCGCGCTGCCCTGATCGAT 960

Qy        961 TGCCTGGCTCCGGATCGTCGTGTAGAGATCGAAGTTAAAGGCTACAAAGAAGTTGTAACT 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TGCCTGGCTCCGGATCGTCGTGTAGAGATCGAAGTTAAAGGCTACAAAGAAGTTGTAACT 1020

Qy       1021 CAGCCGGCGGGT 1032
              |||||   || |
Db       1021 CAGCCTCAGGCT 1032
```

Search completed: January 19, 2005, 15:31:33
Job time : 4775 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: January 19, 2005, 16:38:49 ; Search time 95 Seconds
(without alignments)
2083.462 Million cell updates/sec

Title: US-09-913-772-2
Perfect score: 1823
Sequence: 1 MKAIFVLNAAPKDNTWYAGG.....DRRVEIEVKGYKEVVTQPAG 344

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1813	99.5	344	1	OMPA_KLEPN	P24017 klebsiella
2	1542	84.6	350	1	OMPA_ENTAE	P09146 enterobacte
3	1525.5	83.7	351	1	OMPA_SHIDY	P02935 shigella dy
4	1511	82.9	346	1	OMPA_ECOLI	P02934 escherichia
5	1511	82.9	346	2	Q6W821	Q6w821 shigella so
6	1511	82.9	346	2	AAP74759	Aap74759 shigella
7	1507	82.7	346	2	Q6PNM6	Q6pnm6 shigella bo
8	1507	82.7	346	2	AAT02227	Aat02227 shigella
9	1505	82.6	346	2	Q9L6J0	Q916j0 escherichia
10	1499	82.2	350	2	Q8Z7S0	Q8z7s0 salmonella
11	1495	82.0	350	1	OMPA_SALTY	P02936 salmonella
12	1487	81.6	379	2	Q8CW76	Q8cw76 escherichia
13	1473	80.8	348	2	Q7UD17	Q7ud17 shigella fl
14	1473	80.8	372	2	Q83RX2	Q83rx2 shigella fl
15	1466	80.4	327	2	Q7X0I7	Q7x0i7 shigella fl
16	1381.5	75.8	359	1	OMPA_SERMA	P04845 serratia ma
17	1364	74.8	319	2	Q6QT47	Q6qt47 salmonella
18	1364	74.8	319	2	AAS18468	Aas18468 salmonell
19	1325.5	72.7	353	2	Q8ZG77	Q8zg77 yersinia pe
20	1325.5	72.7	363	2	Q8D056	Q8d056 yersinia pe
21	1325.5	72.7	363	2	AAS61569	Aas61569 yersinia
22	1306	71.6	366	2	Q6D6D4	Q6d6d4 erwinia car
23	1289	70.7	368	2	Q7N602	Q7n602 photorhabdu
24	1262.5	69.3	367	2	Q9RM69	Q9rm69 erwinia car
25	1128.5	61.9	238	2	Q99114	Q99114 escherichia
26	1112.5	61.0	244	2	Q47880	Q47880 escherichia
27	1111	60.9	243	1	OMPA_ESCFE	P24747 escherichia
28	1110.5	60.9	244	2	Q99115	Q99115 escherichia
29	1106	60.7	243	1	OMPA_ESCHE	P24754 escherichia
30	1095.5	60.1	238	2	Q99123	Q99123 enterobacte
31	1089	59.7	241	1	OMPA_ESCBL	Q99124 escherichia
32	1056.5	58.0	238	1	OMPA_CITFR	P24016 citrobacter
33	1042	57.2	249	2	Q9L6I9	Q916i9 salmonella
34	1012	55.5	246	2	Q9L6I8	Q916i8 shigella fl
35	886	48.6	243	1	OMPA_SEROD	P24755 serratia od
36	849	46.6	162	2	Q6WAF8	Q6waf8 klebsiella
37	849	46.6	162	2	AAQ96089	Aaq96089 klebsiell
38	843	46.2	162	2	Q6WAF6	Q6waf6 klebsiella
39	843	46.2	162	2	Q6WAF7	Q6waf7 klebsiella
40	843	46.2	162	2	Q6WAF9	Q6waf9 klebsiella
41	843	46.2	162	2	AAQ96088	Aaq96088 klebsiell
42	843	46.2	162	2	AAQ96090	Aaq96090 klebsiell
43	843	46.2	162	2	AAQ96091	Aaq96091 klebsiell
44	835	45.8	162	2	Q6WAG0	Q6wag0 klebsiella
45	835	45.8	162	2	Q6WAG1	Q6wag1 klebsiella

ALIGNMENTS

RESULT 1
OMPA_KLEPN
ID OMPA_KLEPN STANDARD; PRT; 344 AA.
AC P24017; O69435;
DT 01-MAR-1992 (Rel. 21, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Outer membrane protein A precursor (Outer membrane protein II).
GN Name=ompA;
OS Klebsiella pneumoniae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Klebsiella.
OX NCBI_TaxID=573;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RV 308;
RX MEDLINE=98192544; PubMed=9524233;
RA Nguyen T.N., Samuelson P., Sterky F., Merle-Poitte C., Robert A.,
RA Baussant T., Haeuw J.F., Uhlen M., Binz H., Stahl S.;
RT "Chromosomal sequencing using a PCR-based biotin-capture method
RT allowed isolation of the complete gene for the outer membrane protein
RT A of Klebsiella pneumoniae.";
RL Gene 210:93-101(1998).
RN [2]
RP SEQUENCE OF 93-335 FROM N.A.
RC STRAIN=LD119;
RX MEDLINE=92065252; PubMed=1955870;
RA Lawrence J.G., Ochman H., Hartl D.L.;
RT "Molecular and evolutionary relationships among enteric bacteria.";
RL J. Gen. Microbiol. 137:1911-1921(1991).
CC -!- FUNCTION: Required for the action of colicins K and L and for the
CC stabilization of mating aggregates in conjugation. Serves as a
CC receptor for a number of T-even like phages. Also acts as a porin
CC with low permeability that allows slow penetration of small
CC solutes (By similarity).
CC -!- SUBUNIT: Monomer (Probable).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane.
CC -!- SIMILARITY: Belongs to the ompA family.
CC ---

CC ---
DR EMBL; AJ000998; CAA04450.1; -.
DR EMBL; M63355; AAA25119.1; -.
DR HSSP; P02934; 1QJP.
DR InterPro; IPR006664; Bac_OmpA.
DR InterPro; IPR002368; OmpA.
DR InterPro; IPR006665; OmpA/MotB.
DR InterPro; IPR006690; OMPA_LIKE.

```
DR   InterPro; IPR000498; OmpA_tmem.
DR   Pfam; PF00691; OmpA; 1.
DR   Pfam; PF01389; OmpA_membrane; 1.
DR   PRINTS; PR01021; OMPADOMAIN.
DR   ProDom; PD000930; OmpA/MotB; 1.
DR   PROSITE; PS01068; OMPA; 1.
KW   Conjugation; Outer membrane; Phage recognition; Porin; Repeat; Signal;
KW   Transmembrane.
FT   SIGNAL        1      ?       Potential.
FT   CHAIN         ?    344       Outer membrane protein A.
FT   TRANSMEM     15     28       Potential.
FT   TRANSMEM     48     60       Potential.
FT   TRANSMEM     63     78       Potential.
FT   TRANSMEM     90    100       Potential.
FT   TRANSMEM    104    119       Potential.
FT   TRANSMEM    140    151       Potential.
FT   TRANSMEM    157    173       Potential.
FT   TRANSMEM    179    190       Potential.
FT   DOMAIN      199    206       4 X 2 AA tandem repeats of A-P.
FT   REPEAT      199    200       1.
FT   REPEAT      201    202       2.
FT   REPEAT      203    204       3.
FT   REPEAT      205    206       4.
FT   DOMAIN      255    299       OmpA-like.
FT   DISULFID    309    321       By similarity.
FT   CONFLICT    335    335       Y -> I (in Ref. 2).
SQ   SEQUENCE   344 AA;  37061 MW;  AC88AAE3B7871B16 CRC64;

  Query Match             99.5%;  Score 1813;  DB 1;  Length 344;
  Best Local Similarity   100.0%;  Pred. No. 4.2e-131;
  Matches  342;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MKAIFVLNAAPKDNTWYAGGKLGWSQYHDTGFYGNGFQNNNGPTRNDQLGAGAFGGYQVN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MKAIFVLNAAPKDNTWYAGGKLGWSQYHDTGFYGNGFQNNNGPTRNDQLGAGAFGGYQVN 60

Qy         61 PYLGFEMGYDWLGRMAYKGSVDNGAFKAQGVQLTAKLGYPITDDLDIYTRLGGMVWRADS 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 PYLGFEMGYDWLGRMAYKGSVDNGAFKAQGVQLTAKLGYPITDDLDIYTRLGGMVWRADS 120

Qy        121 KGNYASTGVSRSEHDTGVSPVFAGGVEWAVTRDIATRLEYQWVNNIGDAGTVGTRPDNGM 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 KGNYASTGVSRSEHDTGVSPVFAGGVEWAVTRDIATRLEYQWVNNIGDAGTVGTRPDNGM 180

Qy        181 LSLGVSYRFGQEDAAPVVAPAPAPAPEVATKHFTLKSDVLFNFNKATLKPEGQQALDQLY 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 LSLGVSYRFGQEDAAPVVAPAPAPAPEVATKHFTLKSDVLFNFNKATLKPEGQQALDQLY 240

Qy        241 TQLSNMDPKDGSAVVLGYTDRIGSEAYNQQLSEKRAQSVVDYLVAKGIPAGKISARGMGE 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TQLSNMDPKDGSAVVLGYTDRIGSEAYNQQLSEKRAQSVVDYLVAKGIPAGKISARGMGE 300

Qy        301 SNPVTGNTCDNVKARAALIDCLAPDRRVEIEVKGYKEVVTQP 342
              |||||||||||||||||||||||||||||||||||||||||||
Db        301 SNPVTGNTCDNVKARAALIDCLAPDRRVEIEVKGYKEVVTQP 342


RESULT 2
OMPA_ENTAE
ID   OMPA_ENTAE     STANDARD;      PRT;   350 AA.
AC   P09146;
DT   01-MAR-1989 (Rel. 10, Created)
DT   01-MAR-1989 (Rel. 10, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Outer membrane protein A precursor.
GN   Name=ompA;
OS   Enterobacter aerogenes (Aerobacter aerogenes).
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC   Enterobacteriaceae; Enterobacter.
OX   NCBI_TaxID=548;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=84108348; PubMed=6363059;
RA   Braun G., Cole S.T.;
RT   "Molecular characterization of the gene coding for major outer
RT   membrane protein OmpA from Enterobacter aerogenes.";
RL   Eur. J. Biochem. 137:495-500(1983).
CC   -!- FUNCTION: Required for the action of colicins K and L and for the
CC       stabilization of mating aggregates in conjugation. Serves as a
CC       receptor for a number of T-even like phages. Also acts as a porin
CC       with low permeability that allows slow penetration of small
CC       solutes (By similarity).
CC   -!- SUBUNIT: Monomer (Probable).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane.
CC   -!- SIMILARITY: Belongs to the ompA family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   use by non-profit institutions as long as its content is in no way
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X00254; CAA25062.1; -.
DR   PIR; S07222; S07222.
DR   HSSP; P02934; 1QJP.
DR   InterPro; IPR006664; Bac_OmpA.
DR   InterPro; IPR002368; OmpA.
DR   InterPro; IPR006665; OmpA/MotB.
DR   InterPro; IPR006690; OMPA_LIKE.
DR   InterPro; IPR000498; OmpA_tmem.
DR   Pfam; PF00691; OmpA; 1.
DR   Pfam; PF01389; OmpA_membrane; 1.
DR   PRINTS; PR01021; OMPADOMAIN.
DR   ProDom; PD000930; OmpA/MotB; 1.
DR   PROSITE; PS01068; OMPA; 1.
KW   Conjugation; Outer membrane; Phage recognition; Porin; Repeat; Signal;
KW   Transmembrane.
FT   SIGNAL        1     21
FT   CHAIN        22    350       Outer membrane protein A.
FT   TRANSMEM     27     40       Potential.
FT   TRANSMEM     59     71       Potential.
FT   TRANSMEM     74     89       Potential.
FT   TRANSMEM    101    111       Potential.
FT   TRANSMEM    115    130       Potential.
FT   TRANSMEM    146    157       Potential.
FT   TRANSMEM    163    179       Potential.
FT   TRANSMEM    185    196       Potential.
FT   DOMAIN      205    212       4 X 2 AA tandem repeats of A-P.
FT   REPEAT      205    206       1.
FT   REPEAT      207    208       2.
FT   REPEAT      209    210       3.
FT   REPEAT      211    212       4.
FT   DOMAIN      261    305       OmpA-like.
FT   DISULFID    315    327       By similarity.
SQ   SEQUENCE   350 AA;  37575 MW;  6276C6F2F21065DA CRC64;

  Query Match             84.6%;  Score 1542;  DB 1;  Length 350;
  Best Local Similarity   87.5%;  Pred. No. 3e-110;
  Matches  295;  Conservative   10;  Mismatches   26;  Indels    6;  Gaps    2;

Qy          6 VLNAAPKDNTWYAGGKLGWSQYHDTGFYGNGFQNNNGPTRNDQLGAGAFGGYQVNPYLGF 65
              | |||||||||||||||||:||||:| |    ||||||   ||||||||||||||||||
Db         18 VAQAAPKDNTWYAGGKLGWSQFHDTGWY-NSNLNNNGPTHESQLGAGAFGGYQVNPYLGF 76

Qy         66 EMGYDWLGRMAYKGSVDNGAFKAQGVQLTAKLGYPITDDLDIYTRLGGMVWRADSKGNYA 125
              |||||||||| |||    |||| :| ||||||||||||||||||||||||||||||
Db         77 EMGYDWLGRMPYKGVKVNGAFSSQAVQLTAKLGYPITDDLDIYTRLGGMVWRADS----- 131

Qy        126 STGVSRSEHDTGVSPVFAGGVEWAVTRDIATRLEYQWVNNIGDAGTVGTRPDNGMLSLGV 185
              |  ::   ||||||||||||||:|||||||||||||||||||| |||||||:||
Db        132 SNSIAGDNHDTGVSPVFAGGVEWAMTRDIATRLEYQWVNNIGDAGTVGVRPDNGMLSVGV 191

Qy        186 SYRFGQEDAAPVVAPAPAPAPEVATKHFTLKSDVLFNFNKATLKPEGQQALDQLYTQLSN 245
              ||||||| |||||||||||||| || ||||||||||||||||||||||||||||||||||
```

```
Db        192 SYRFGQEDNAPVVAPAPAPAPEVTTKTFTLKSDVLFNFNKATLKPEGQQALDQLYTQLSN 251

Qy        246 MDPKDGSAVVLGYTDRIGSEAYNQQLSEKRAQSVVDYLVAKGIPAGKISARGMGESNPVT 305
              |||||||||||||||||||| |||:||||||||||||||||||| ||||||||||:|||
Db        252 MDPKDGSAVVLGYTDRIGSEQYNQKLSEKRAQSVVDYLVAKGIPANKISARGMGESDPVT 311

Qy        306 GNTCDNVKARAALIDCLAPDRRVEIEVKGYKEVVTQP 342
              |||||||||||||||||||| |||||||:|||||
Db        312 GNTCDNVKARAALIDCLAPDRRVAIEVKGYKDVVTQP 348


RESULT 3
OMPA_SHIDY
ID   OMPA_SHIDY     STANDARD;      PRT;   351 AA.
AC   P02935;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Outer membrane protein A precursor (Outer membrane protein II).
GN   Name=ompA;
OS   Shigella dysenteriae.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC   Enterobacteriaceae; Shigella.
OX   NCBI_TaxID=622;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=82221414; PubMed=6283478;
RA   Braun G., Cole S.T.;
RT   "The nucleotide sequence coding for major outer membrane protein OmpA
RT   of Shigella dysenteriae.";
RL   Nucleic Acids Res. 10:2367-2378(1982).
CC   -!- FUNCTION: Required for the action of colicins K and L and for the
CC       stabilization of mating aggregates in conjugation. Serves as a
CC       receptor for a number of T-even like phages. Also acts as a porin
CC       with low permeability that allows slow penetration of small
CC       solutes (By similarity).
CC   -!- SUBUNIT: Monomer (Probable).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane.
CC   -!- SIMILARITY: Belongs to the ompA family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; V01344; CAA24638.1; -.
DR   PIR; A03435; MMEBAD.
DR   HSSP; P02934; 1QJP.
DR   InterPro; IPR006664; Bac_OmpA.
DR   InterPro; IPR002368; OmpA.
DR   InterPro; IPR006665; OmpA/MotB.
DR   InterPro; IPR006690; OMPA_LIKE.
DR   InterPro; IPR000498; OmpA_tmem.
DR   Pfam; PF00691; OmpA; 1.
DR   Pfam; PF01389; OmpA_membrane; 1.
DR   PRINTS; PR01021; OMPADOMAIN.
DR   ProDom; PD000930; OmpA/MotB; 1.
DR   PROSITE; PS01068; OMPA; 1.
KW   Conjugation; Outer membrane; Phage recognition; Porin; Repeat; Signal;
KW   Transmembrane.
FT   SIGNAL        1     21
FT   CHAIN        22    351       Outer membrane protein A.
FT   TRANSMEM     27     40       Potential.
FT   TRANSMEM     55     67       Potential.
FT   TRANSMEM     70     85       Potential.
FT   TRANSMEM     97    107       Potential.
FT   TRANSMEM    111    126       Potential.
FT   TRANSMEM    147    158       Potential.
FT   TRANSMEM    164    180       Potential.
FT   TRANSMEM    186    197       Potential.
FT   DOMAIN      206    213       4 X 2 AA tandem repeats of A-P.
FT   REPEAT      206    207       1.
FT   REPEAT      208    209       2.
FT   REPEAT      210    211       3.
FT   REPEAT      212    213       4.
FT   DOMAIN      262    306       OmpA-like.
FT   DISULFID    316    328       By similarity.
SQ   SEQUENCE   351 AA;  37741 MW;  1499AA5F5395B35B CRC64;

  Query Match           83.7%;  Score 1525.5;  DB 1;  Length 351;
  Best Local Similarity  84.6%;  Pred. No. 5.6e-109;
  Matches  285;  Conservative   20;  Mismatches   27;  Indels    5;  Gaps    1;

Qy          6 VLNAAPKDNTWYAGGKLGWSQYHDTGFYGNGFQNNNGPTRNDQLGAGAFGGYQVNPYLGF 65
              |  ||||||||| | ||||||||||||      :|||||  :||||||||||||||:||
Db         18 VAQAAPKDNTWYTGAKLGWSQYHDTGFI-----DNNGPTHENQLGAGAFGGYQVNPYVGF 72

Qy         66 EMGYDWLGRMAYKGSVDNGAFKAQGVQLTAKLGYPITDDLDIYTRLGGMVWRADSKGNYA 125
              |||||||||| |||||:|||:||||||||||||||||||:||||||||||||:|·:
Db         73 EMGYDWLGRMPYKGSVENGAYKAQGVQLTAKLGYPITDDLDVYTRLGGMVWRADTKAHNN 132

Qy        126 STGVSRSEHDTGVSPVFAGGVEWAVTRDIATRLEYQWVNNIGDAGTVGTRPDNGMLSLGV 185
              || |   |||||||||||||||:| :||||||||| ||||||  |:|||||||:|||||
Db        133 VTGESEKNHDTGVSPVFAGGVEWAITPEIATRLEYQWTNNIGDAHTIGTRPDNGLLSLGV 192

Qy        186 SYRFGQEDAAPVVAPAPAPAPEVATKHFTLKSDVLFNFNKATLKPEGQQALDQLYTQLSN 245
              |||||| :|||||||||||||| ||||||||||||||||||||||| ||||||:||||
Db        193 SYRFGQGEAAPVVAPAPAPAPEVQTKHFTLKSDVLFNFNKATLKPEGQAALDQLYSQLSN 252

Qy        246 MDPKDGSAVVLGYTDRIGSEAYNQQLSEKRAQSVVDYLVAKGIPAGKISARGMGESNPVT 305
              :|||||| ||||||||||:|||| |||:|||||||::||||| ||||||||||||||
Db        253 LDPKDGSVVVLGYTDRIGSDAYNQGLSERRAQSVVDYLISKGIPADKISARGMGESNPVT 312

Qy        306 GNTCDNVKARAALIDCLAPDRRVEIEVKGYKEVVTQP 342
              |||||||| |||||||||||||||||||| |:|||||
Db        313 GNTCDNVKQRAALIDCLAPDRRVEIEVKGIKDVVTQP 349


RESULT 4
OMPA_ECOLI
ID   OMPA_ECOLI     STANDARD;      PRT;   346 AA.
AC   P02934;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   01-OCT-2004 (Rel. 45, Last annotation update)
DE   Outer membrane protein A precursor (Outer membrane protein II*).
GN   Name=ompA; Synonyms=tolG, tut, con;
GN   OrderedLocusNames=b0957, z1307, ECs1041;
OS   Escherichia coli, and
OS   Escherichia coli O157:H7.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC   Enterobacteriaceae; Escherichia.
OX   NCBI_TaxID=562, 83334;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=K12;
RX   MEDLINE=81053729; PubMed=6253901;
RA   Beck E., Bremer E.;
RT   "Nucleotide sequence of the gene ompA coding the outer membrane
RT   protein II of Escherichia coli K-12.";
RL   Nucleic Acids Res. 8:3011-3024(1980).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=K12;
RX   MEDLINE=81170587; PubMed=6260961;
RA   Movva N.R., Nakamura K., Inouye M.;
RT   "Gene structure of the OmpA protein, a major surface protein of
RT   Escherichia coli required for cell-cell interaction.";
RL   J. Mol. Biol. 143:317-328(1980).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=K12 / MG1655;
RX   MEDLINE=97426617; PubMed=9278503;
```

RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=97061202; PubMed=8905232;
RA Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,
RA Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
RA Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
RA Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N.,
RA Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
RA Yano M., Horiuchi T.;
RT "A 718-kb DNA sequence of the Escherichia coli K-12 genome
RT corresponding to the 12.7-28.0 min region on the linkage map.";
RL DNA Res. 3:137-155(1996).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / EDL933 / ATCC 700927 / EHEC;
RX MEDLINE=21074935; PubMed=11206551; DOI=10.1038/35054089;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
RL Nature 409:529-533(2001).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / RIMD 0509952 / EHEC;
RX MEDLINE=21156231; PubMed=11258796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;
RT "Complete genome sequence of enterohemorrhagic Escherichia coli
RT O157:H7 and genomic comparison with a laboratory strain K-12.";
RL DNA Res. 8:11-22(2001).
RN [7]
RP SEQUENCE OF 22-346.
RC STRAIN=K12;
RX MEDLINE=81054820; PubMed=7001461;
RA Chen R., Schmidmayr W., Kramer C., Chen-Schmeisser U., Henning U.;
RT "Primary structure of major outer membrane protein II (ompA protein)
RT of Escherichia coli K-12.";
RL Proc. Natl. Acad. Sci. U.S.A. 77:4592-4596(1980).
RN [8]
RP SEQUENCE OF 22-32.
RC STRAIN=K12 / W3110;
RA Pasquali C., Sanchez J.-C., Ravier F., Golaz O., Hughes G.J.,
RA Frutiger S., Paquet N., Wilkins M., Appel R.D., Bairoch A.,
RA Hochstrasser D.F.;
RL Submitted (SEP-1994) to Swiss-Prot.
RN [9]
RP SEQUENCE OF 22-34.
RC STRAIN=K12 / EMG2;
RX MEDLINE=97443975; PubMed=9298646;
RA Link A.J., Robison K., Church G.M.;
RT "Comparing the predicted and observed properties of proteins encoded
RT in the genome of Escherichia coli K-12.";
RL Electrophoresis 18:1259-1313(1997).
RN [10]
RP SEQUENCE OF 22-26.
RC STRAIN=K12 / W3110;
RX MEDLINE=98291876; PubMed=9629924;
RA Molloy M.P., Herbert B.R., Walsh B.J., Tyler M.I., Traini M.,
RA Sanchez J.-C., Hochstrasser D.F., Williams K.L., Gooley A.A.;
RT "Extraction of membrane proteins by differential solubilization for
RT separation using two-dimensional gel electrophoresis.";
RL Electrophoresis 19:837-844(1998).
RN [11]
RP MUTANTS RESISTANT TO PHAGE ENTRY.
RX MEDLINE=84264337; PubMed=6086577;
RA Morona R., Klose M., Henning U.;
RT "Escherichia coli K-12 outer membrane protein (OmpA) as a
RT bacteriophage receptor: analysis of mutant genes expressing altered
RT proteins.";
RL J. Bacteriol. 159:570-578(1984).
RN [12]
RP MUTANTS RESISTANT TO PHAGE ENTRY.
RX MEDLINE=86033606; PubMed=3902787;
RA Morona R., Kramer C., Henning U.;
RT "Bacteriophage receptor area of outer membrane protein OmpA of
RT Escherichia coli K-12.";
RL J. Bacteriol. 164:539-543(1985).
RN [13]
RP PORIN ACTIVITY.
RC STRAIN=K12;
RX MEDLINE=92129334; PubMed=1370823;
RA Sugawara E., Nikaido H.;
RT "Pore-forming activity of OmpA protein of Escherichia coli.";
RL J. Biol. Chem. 267:2507-2511(1992).
RN [14]
RP SUBCELLULAR LOCATION.
RX PubMed=7813480;
RA Kuhn A., Kiefer D., Koehne C., Zhu H.-Y., Tschantz W.R., Dalbey R.E.;
RT "Evidence for a loop-like insertion mechanism of pro-Omp A into the
RT inner membrane of Escherichia coli.";
RL Eur. J. Biochem. 226:891-897(1994).
RN [15]
RP TOPOLOGY.
RX MEDLINE=94148615; PubMed=8106193;
RA Gromiha M.M., Ponnuswamy P.K.;
RT "Prediction of transmembrane beta-strands from hydrophobic
RT characteristics of proteins.";
RL Int. J. Pept. Protein Res. 42:420-431(1993).
RN [16]
RP TOPOLOGY.
RX MEDLINE=99296577; PubMed=10368142;
RA Koebnik R.;
RT "Structural and functional roles of the surface-exposed loops of the
RT beta-barrel membrane protein OmpA from Escherichia coli.";
RL J. Bacteriol. 181:3688-3694(1999).
RN [17]
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 22-192.
RX MEDLINE=99023200; PubMed=9808047;
RA Pautsch A., Schulz G.E.;
RT "Structure of the outer membrane protein A transmembrane domain.";
RL Nat. Struct. Biol. 5:1013-1017(1998).
RN [18]
RP X-RAY CRYSTALLOGRAPHY (1.65 ANGSTROMS).
RX MEDLINE=20229895; PubMed=10764596;
RA Pautsch A., Schulz G.E.;
RT "High-resolution structure of the OmpA membrane domain.";
RL J. Mol. Biol. 298:273-282(2000).
RN [19]
RP STRUCTURE BY NMR OF 22-197.
RX PubMed=11276254; DOI=10.1038/86214;
RA Arora A., Abildgaard F., Bushweller J.H., Tamm L.K.;
RT "Structure of outer membrane protein A transmembrane domain by NMR
RT spectroscopy.";
RL Nat. Struct. Biol. 8:334-338(2001).
RN [20]
RP MASS SPECTROMETRY.
RX MEDLINE=20222957; PubMed=10757971;
RA le Coutre J., Whitelegge J.P., Gross A., Turk E., Wright E.M.,
RA Kaback H.R., Faull K.F.;
RT "Proteomics on full-length membrane proteins using mass
RT spectrometry.";
RL Biochemistry 39:4237-4242(2000).
CC -!- FUNCTION: Required for the action of colicins K and L and for the
CC stabilization of mating aggregates in conjugation. Serves as a

```
CC       receptor for a number of T-even like phages. Also acts as a porin
CC       with low permeability that allows slow penetration of small
CC       solutes.
CC   -!- SUBUNIT: Monomer (Probable).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane.
CC   -!- MASS SPECTROMETRY: MW=35177; METHOD=Electrospray; RANGE=22-346;
CC       NOTE=Ref.20.
CC   -!- SIMILARITY: Belongs to the ompA family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; V00307; CAA23588.1; -.
DR   EMBL; AE000198; AAC74043.1; -.
DR   EMBL; D90733; BAA35715.1; -.
DR   EMBL; D90734; BAA35722.1; -.

  Query Match             82.9%;  Score 1511;  DB 1;  Length 346;
  Best Local Similarity   84.9%;  Pred. No. 7.1e-108;
  Matches  286;  Conservative   17;  Mismatches   24;  Indels   10;  Gaps    2;

Qy          6 VLNAAPKDNTWYAGGKLGWSQYHDTGFYGNGFQNNNGPTRNDQLGAGAFGGYQVNPYLGF 65
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Db         18 VAQAAPKDNTWYTGAKLGWSQYHDTGFI-----NNNGPTHENQLGAGAFGGYQVNPYVGF 72

Qy         66 EMGYDWLGRMAYKGSVDNGAFKAQGVQLTAKLGYPITDDLDIYTRLGGMVWRADSKGNYA 125
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Db         73 EMGYDWLGRMPYKGSVENGAYKAQGVQLTAKLGYPITDDLDIYTRLGGMVWRADTKSN-- 130

Qy        126 STGVSRSEHDTGVSPVFAGGVEWAVTRDIATRLEYQWVNNIGDAGTVGTRPDNGMLSLGV 185
                  |    ||||||||||||||:|:| :|||||||| |||||| |:|||||||||||||
Db        131 ---VYGKNHDTGVSPVFAGGVEYAITPEIATRLEYQWTNNIGDAHTIGTRPDNGMLSLGV 187

Qy        186 SYRFGQEDAAPVVAPAPAPAPEVATKHFTLKSDVLFNFNKATLKPEGQQALDQLYTQLSN 245
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Db        188 SYRFGQGEAAPVVAPAPAPAPEVQTKHFTLKSDVLFNFNKATLKPEGQAALDQLYSQLSN 247

Qy        246 MDPKDGSAVVLGYTDRIGSEAYNQQLSEKRAQSVVDYLVAKGIPAGKISARGMGESNPVT 305
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Db        248 LDPKDGSVVVLGYTDRIGSDAYNQGLSERRAQSVVDYLISKGIPADKISARGMGESNPVT 307

Qy        306 GNTCDNVKARAALIDCLAPDRRVEIEVKGYKEVVTQP 342
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Db        308 GNTCDNVKQRAALIDCLAPDRRVEIEVKGIKDVVTQP 344


RESULT 5
Q6W821
ID   Q6W821      PRELIMINARY;      PRT;   346 AA.
AC   Q6W821;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Outer membrane protein A precursor.
GN   Name=ompA;
OS   Shigella sonnei.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC   Enterobacteriaceae; Shigella.
OX   NCBI_TaxID=624;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=USMSS2;
RA   Kirnpal-Kaur B., Mohd Zaki S., Asma I., Ravichandran M.;
RL   Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Belongs to the ompA family.
DR   EMBL; AY305874; AAP74759.1; -.
DR   InterPro; IPR006664; Bac_OmpA.
DR   InterPro; IPR001035; MotY.
DR   InterPro; IPR002368; OmpA.
DR   InterPro; IPR006665; OmpA/MotB.
DR   InterPro; IPR006690; OMPA_LIKE.
DR   InterPro; IPR000498; OmpA_tmem.
DR   Pfam; PF00691; OmpA; 1.
DR   Pfam; PF01389; OmpA_membrane; 1.
DR   PRINTS; PR01023; NAFLGMOTY.
DR   PRINTS; PR01021; OMPADOMAIN.
DR   PRINTS; PR01022; OUTRMMBRANEA.
DR   ProDom; PD000930; OmpA/MotB; 1.
DR   PROSITE; PS01068; OMPA; 1.
KW   Signal.
FT   SIGNAL        1     21       Potential.
SQ   SEQUENCE   346 AA;  37201 MW;  195147734CDF8B04 CRC64;

  Query Match             82.9%;  Score 1511;  DB 2;  Length 346;
  Best Local Similarity   84.9%;  Pred. No. 7.1e-108;
  Matches  286;  Conservative   17;  Mismatches   24;  Indels   10;  Gaps    2;

Qy          6 VLNAAPKDNTWYAGGKLGWSQYHDTGFYGNGFQNNNGPTRNDQLGAGAFGGYQVNPYLGF 65
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Qy         66 EMGYDWLGRMAYKGSVDNGAFKAQGVQLTAKLGYPITDDLDIYTRLGGMVWRADSKGNYA 125
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Qy        126 STGVSRSEHDTGVSPVFAGGVEWAVTRDIATRLEYQWVNNIGDAGTVGTRPDNGMLSLGV 185
                  |    ||||||||||||||:|:| :|||||||| |||||| |:|||||||||||||
Db        131 ---VYGKNHDTGVSPVFAGGVEYAITPEIATRLEYQWTNNIGDAHTIGTRPDNGMLSLGV 187

Qy        186 SYRFGQEDAAPVVAPAPAPAPEVATKHFTLKSDVLFNFNKATLKPEGQQALDQLYTQLSN 245
              |||||| :|||||||||||||| |||||||||||||||||||||| ||||||:||||
Db        188 SYRFGQGEAAPVVAPAPAPAPEVQTKHFTLKSDVLFNFNKATLKPEGQAALDQLYSQLSN 247

Qy        246 MDPKDGSAVVLGYTDRIGSEAYNQQLSEKRAQSVVDYLVAKGIPAGKISARGMGESNPVT 305
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Db        248 LDPKDGSVVVLGYTDRIGSDAYNQGLSERRAQSVVDYLISKGIPADKISARGMGESNPVT 307

Qy        306 GNTCDNVKARAALIDCLAPDRRVEIEVKGYKEVVTQP 342
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Db        308 GNTCDNVKQRAALIDCLAPDRRVEIEVKGIKDVVTQP 344


RESULT 6
AAP74759
ID   AAP74759    PRELIMINARY;      PRT;   346 AA.
AC   AAP74759;
DT   02-MAR-2004 (TrEMBLrel. 27, Created)
DT   02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT   02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE   Outer membrane protein A precursor.
GN   OMPA.
OS   Shigella sonnei.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC   Enterobacteriaceae; Shigella.
OX   NCBI_TaxID=624;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=USMSS2;
RA   Kirnpal-Kaur B., Mohd Zaki S., Asma I., Ravichandran M.;
RL   Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY305874; AAP74759.1; -.
KW   Signal.
FT   SIGNAL        1     21       Potential.
SQ   SEQUENCE   346 AA;  37201 MW;  195147734CDF8B04 CRC64;

  Query Match             82.9%;  Score 1511;  DB 2;  Length 346;
  Best Local Similarity   84.9%;  Pred. No. 7.1e-108;
  Matches  286;  Conservative   17;  Mismatches   24;  Indels   10;  Gaps    2;

Qy          6 VLNAAPKDNTWYAGGKLGWSQYHDTGFYGNGFQNNNGPTRNDQLGAGAFGGYQVNPYLGF 65
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Db         18 VAQAAPKDNTWYTGAKLGWSQYHDTGFI-----NNNGPTHENQLGAGAFGGYQVNPYVGF 72

Qy         66 EMGYDWLGRMAYKGSVDNGAFKAQGVQLTAKLGYPITDDLDIYTRLGGMVWRADSKGNYA 125
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Db         73 EMGYDWLGRMPYKGSVENGAYKAQGVQLTAKLGYPITDDLDIYTRLGGMVWRADTKSN-- 130

Qy        126 STGVSRSEHDTGVSPVFAGGVEWAVTRDIATRLEYQWVNNIGDAGTVGTRPDNGMLSLGV 185
                 |    |||||||||||||||:|:| :|||||||| |||||| |:||||||||||||
Db        131 ---VYGKNHDTGVSPVFAGGVEYAITPEIATRLEYQWTNNIGDAHTIGTRPDNGMLSLGV 187

Qy        186 SYRFGQEDAAPVVAPAPAPAPEVATKHFTLKSDVLFNFNKATLKPEGQQALDQLYTQLSN 245
              |||||| :|||||||||||||| |||||||||||||||||||||| ||||||:||||
Db        188 SYRFGQGEAAPVVAPAPAPAPEVQTKHFTLKSDVLFNFNKATLKPEGQAALDQLYSQLSN 247

Qy        246 MDPKDGSAVVLGYTDRIGSEAYNQQLSEKRAQSVVDYLVAKGIPAGKISARGMGESNPVT 305
              :|||||| |||||||||||:|||| |||:|||||||||::|||||  ||||||||||||||
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Qy        306 GNTCDNVKARAALIDCLAPDRRVEIEVKGYKEVVTQP 342
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Db        308 GNTCDNVKQRAALIDCLAPDRRVEIEVKGIKDVVTQP 344


RESULT 7
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ID   Q6PNM6      PRELIMINARY;      PRT;   346 AA.
AC   Q6PNM6;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Outer membrane protein A precursor.
GN   Name=ompA;
OS   Shigella boydii.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC   Enterobacteriaceae; Shigella.
OX   NCBI_TaxID=621;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=MalaysiaSB631;
RA   Nik Noorul Shakira M.S., Kirnpal-Kaur B.S., Ravichandran M., Asma I.,
RA   Mohd Zaki S.;
RL   Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Belongs to the ompA family.
DR   EMBL; AY590298; AAT02227.1; -.
DR   InterPro; IPR006664; Bac_OmpA.
DR   InterPro; IPR001035; MotY.
DR   InterPro; IPR002368; OmpA.
DR   InterPro; IPR006665; OmpA/MotB.
DR   InterPro; IPR006690; OMPA_LIKE.
DR   InterPro; IPR000498; OmpA_tmem.
DR   Pfam; PF00691; OmpA; 1.
DR   Pfam; PF01389; OmpA_membrane; 1.
DR   PRINTS; PR01023; NAFLGMOTY.
DR   PRINTS; PR01021; OMPADOMAIN.
DR   PRINTS; PR01022; OUTRMMBRANEA.
DR   ProDom; PD000930; OmpA/MotB; 1.
DR   PROSITE; PS01068; OMPA; 1.
KW   Signal.
FT   SIGNAL       1     21       Potential.
SQ   SEQUENCE   346 AA;  37229 MW;  E94650734CDF9239 CRC64;

  Query Match             82.7%;  Score 1507;  DB 2;  Length 346;
  Best Local Similarity   84.6%;  Pred. No. 1.4e-107;
  Matches  285;  Conservative   17;  Mismatches   25;  Indels   10;  Gaps    2;

Qy          6 VLNAAPKDNTWYAGGKLGWSQYHDTGFYGNGFQNNNGPTRNDQLGAGAFGGYQVNPYLGF 65
              |  ||||||||| | ||||||||||||      ||||||  :|||||||||||||:||
Db         18 VAQAAPKDNTWYTGAKLGWSQYHDTGFI-----NNNGPTHENQLGAGAFGGYQVNPYVGF 72

Qy         66 EMGYDWLGRMAYKGSVDNGAFKAQGVQLTAKLGYPITDDLDIYTRLGGMVWRADSKGNYA 125
              |||||||||| |||||:|||:||||||||||||||||||||||||||||||||:| |
Db         73 EMGYDWLGRMPYKGSVENGAYKAQGVQLTAKLGYPITDDLDIYTRLGGMVWRADTKSN-- 130

Qy        126 STGVSRSEHDTGVSPVFAGGVEWAVTRDIATRLEYQWVNNIGDAGTVGTRPDNGMLSLGV 185
                 |    |||||||||||||||:|:| :|||||||| |||||| |:||||||||||||
Db        131 ---VYGKNHDTGVSPVFAGGVEYAITPEIATRLEYQWTNNIGDAHTIGTRPDNGMLSLGV 187

Qy        186 SYRFGQEDAAPVVAPAPAPAPEVATKHFTLKSDVLFNFNKATLKPEGQQALDQLYTQLSN 245
              |||||| :|||||||||||||| |||||||||||||||||||||| ||||||:||||
Db        188 SYRFGQGEAAPVVAPAPAPAPEVQTKHFTLKSDVLFNFNKATLKPEGQAALDQLYSQLSN 247

Qy        246 MDPKDGSAVVLGYTDRIGSEAYNQQLSEKRAQSVVDYLVAKGIPAGKISARGMGESNPVT 305
              :|||||| |||||||||||:|||| |||:|||||||||::|||||  ||||||||||||||
Db        248 LDPKDGSVVVLGYTDRIGSDAYNQGLSERRAQSVVDYLISKGIPVDKISARGMGESNPVT 307

Qy        306 GNTCDNVKARAALIDCLAPDRRVEIEVKGYKEVVTQP 342
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Db        308 GNTCDNVKQRAALIDCLAPDRRVEIEVKGIKDVVTQP 344


RESULT 8
AAT02227
ID   AAT02227    PRELIMINARY;      PRT;   346 AA.
AC   AAT02227;
DT   10-MAY-2004 (TrEMBLrel. 27, Created)
DT   10-MAY-2004 (TrEMBLrel. 27, Last sequence update)
DT   10-MAY-2004 (TrEMBLrel. 27, Last annotation update)
DE   Outer membrane protein A precursor.
GN   OMPA.
OS   Shigella boydii.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC   Enterobacteriaceae; Shigella.
OX   NCBI_TaxID=621;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=MalaysiaSB631;
RA   Nik Noorul Shakira M.S., Kirnpal-Kaur B.S., Ravichandran M., Asma I.,
RA   Mohd Zaki S.;
RT   "Shigella boydii outer membrane protein A precursor (ompA) gene.";
RL   Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY590298; AAT02227.1; -.
KW   Signal.
FT   SIGNAL       1     21       Potential.
SQ   SEQUENCE   346 AA;  37229 MW;  E94650734CDF9239 CRC64;

  Query Match             82.7%;  Score 1507;  DB 2;  Length 346;
  Best Local Similarity   84.6%;  Pred. No. 1.4e-107;
  Matches  285;  Conservative   17;  Mismatches   25;  Indels   10;  Gaps    2;

Qy          6 VLNAAPKDNTWYAGGKLGWSQYHDTGFYGNGFQNNNGPTRNDQLGAGAFGGYQVNPYLGF 65
              |  ||||||||| | ||||||||||||      ||||||  :|||||||||||||:||
Db         18 VAQAAPKDNTWYTGAKLGWSQYHDTGFI-----NNNGPTHENQLGAGAFGGYQVNPYVGF 72

Qy         66 EMGYDWLGRMAYKGSVDNGAFKAQGVQLTAKLGYPITDDLDIYTRLGGMVWRADSKGNYA 125
              |||||||||| |||||:|||:||||||||||||||||||||||||||||||||:| |
Db         73 EMGYDWLGRMPYKGSVENGAYKAQGVQLTAKLGYPITDDLDIYTRLGGMVWRADTKSN-- 130

Qy        126 STGVSRSEHDTGVSPVFAGGVEWAVTRDIATRLEYQWVNNIGDAGTVGTRPDNGMLSLGV 185
                 |    |||||||||||||||:|:| :|||||||| |||||| |:||||||||||||
Db        131 ---VYGKNHDTGVSPVFAGGVEYAITPEIATRLEYQWTNNIGDAHTIGTRPDNGMLSLGV 187

Qy        186 SYRFGQEDAAPVVAPAPAPAPEVATKHFTLKSDVLFNFNKATLKPEGQQALDQLYTQLSN 245
              |||||| :|||||||||||||| |||||||||||||||||||||| ||||||:||||
Db        188 SYRFGQGEAAPVVAPAPAPAPEVQTKHFTLKSDVLFNFNKATLKPEGQAALDQLYSQLSN 247

Qy        246 MDPKDGSAVVLGYTDRIGSEAYNQQLSEKRAQSVVDYLVAKGIPAGKISARGMGESNPVT 305
              :|||||| |||||||||||:|||| |||:|||||||||::|||||  ||||||||||||||
Db        248 LDPKDGSVVVLGYTDRIGSDAYNQGLSERRAQSVVDYLISKGIPVDKISARGMGESNPVT 307

Qy        306 GNTCDNVKARAALIDCLAPDRRVEIEVKGYKEVVTQP 342
              |||||||| |||||||||||||||||||| |:|||||
Db        308 GNTCDNVKQRAALIDCLAPDRRVEIEVKGIKDVVTQP 344


RESULT 9
Q9L6J0
```

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ID   Q9L6J0      PRELIMINARY;      PRT;   346 AA.
AC   Q9L6J0;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Outer membrane protein A.
GN   Name=ompA;
OS   Escherichia coli.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC   Enterobacteriaceae; Escherichia.
OX   NCBI_TaxID=562;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=RS218;
RA   Wang Y., Kim K.S.;
RL   Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Belongs to the ompA family.
DR   EMBL; AF234269; AAF37887.1; -.
DR   HSSP; P02934; 1QJP.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0009279; C:outer membrane (sensu Gram-negative Bacteria); IEA.
DR   GO; GO:0005198; F:structural molecule activity; IEA.
DR   InterPro; IPR006664; Bac_OmpA.
DR   InterPro; IPR002368; OmpA.
DR   InterPro; IPR006665; OmpA/MotB.
DR   InterPro; IPR006690; OMPA_LIKE.
DR   InterPro; IPR000498; OmpA_tmem.
DR   Pfam; PF00691; OmpA; 1.
DR   Pfam; PF01389; OmpA_membrane; 1.
DR   PRINTS; PR01021; OMPADOMAIN.
DR   PRINTS; PR01022; OUTRMMBRANEA.
DR   ProDom; PD000930; OmpA/MotB; 1.
DR   PROSITE; PS01068; OMPA; 1.
SQ   SEQUENCE   346 AA;  37188 MW;  5736077E41BD84C3 CRC64;

  Query Match             82.6%;  Score 1505;  DB 2;  Length 346;
  Best Local Similarity   84.3%;  Pred. No. 2.1e-107;
  Matches  284;  Conservative   18;  Mismatches   25;  Indels   10;  Gaps    2;

Qy          6 VLNAAPKDNTWYAGGKLGWSQYHDTGFYGNGFQNNNGPTRNDQLGAGAFGGYQVNPYLGF 65
              |  |||||||| | ||||||||||      ||||||  :|||||||||||||||:||
Db         18 VAQAAPKDNTWYTGAKLGWSQYHDTGFI-----NNNGPTHENQLGAGAFGGYQVNPYVGF 72

Qy         66 EMGYDWLGRMAYKGSVDNGAFKAQGVQLTAKLGYPITDDLDIYTRLGGMVWRADSKGNYA 125
              |||||||||| |||||:|||:||||||||||||||||||:||||||||||||:| |
Db         73 EMGYDWLGRMPYKGSVENGAYKAQGVQLTAKLGYPITDDLDVYTRLGGMVWRADTKSN-- 130

Qy        126 STGVSRSEHDTGVSPVFAGGVEWAVTRDIATRLEYQWVNNIGDAGTVGTRPDNGMLSLGV 185
                |  ||||||||||||||:|:| :|||||||| |||||| |:||||||||||||
Db        131 ---VYGKNHDTGVSPVFAGGVEYAITPEIATRLEYQWTNNIGDAHTIGTRPDNGMLSLGV 187

Qy        186 SYRFGQEDAAPVVAPAPAPAPEVATKHFTLKSDVLFNFNKATLKPEGQQALDQLYTQLSN 245
              |||||| :|||||||||||||| |||||||||| |||||||||| |||||||:||||
Db        188 SYRFGQGEAAPVVAPAPAPAPEVQTKHFTLKSDVLFTFNKATLKPEGQAALDQLYSQLSN 247

Qy        246 MDPKDGSAVVLGYTDRIGSEAYNQQLSEKRAQSVVDYLVAKGIPAGKISARGMGESNPVT 305
              :|||||| |||||||||||:|||| |||:|||||||||::||||| ||||||||||||||
Db        248 LDPKDGSVVVLGYTDRIGSDAYNQALSERRAQSVVDYLISKGIPADKISARGMGESNPVT 307

Qy        306 GNTCDNVKARAALIDCLAPDRRVEIEVKGYKEVVTQP 342
              |||||||| |||||||||||||||||||| |:|||||
Db        308 GNTCDNVKQRAALIDCLAPDRRVEIEVKGIKDVVTQP 344


RESULT 10
Q8Z7S0
ID   Q8Z7S0      PRELIMINARY;      PRT;   350 AA.
AC   Q8Z7S0; Q7C962;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Outer membrane protein A.
GN   Name=ompA; OrderedLocusNames=STY1091, t1850;
OS   Salmonella typhi.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC   Enterobacteriaceae; Salmonella.
OX   NCBI_TaxID=601;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CT18;
RX   MEDLINE=21534947; PubMed=11677608; DOI=10.1038/35101607;
RA   Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
RA   Churcher C.M., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M.,
RA   Baker S., Basham D., Brooks K., Chillingworth T., Connerton P.,
RA   Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA   Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
RA   Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
RA   Quail M.A., Rutherford K.M., Simmonds M., Skelton J., Stevens K.,
RA   Whitehead S., Barrell B.G.;
RT   "Complete genome sequence of a multiple drug resistant Salmonella
RT   enterica serovar Typhi CT18.";
RL   Nature 413:848-852(2001).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Ty2 / ATCC 700931;
RX   MEDLINE=22531367; PubMed=12644504;
RA   Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
RA   Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
RT   "Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
RT   and CT18.";
RL   J. Bacteriol. 185:2330-2337(2003).
CC   -!- SIMILARITY: Belongs to the ompA family.
DR   EMBL; AL627269; CAD08196.1; -.
DR   EMBL; AE016840; AAO69468.1; -.
DR   HSSP; P02934; 1QJP.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0009279; C:outer membrane (sensu Gram-negative Bacteria); IEA.
DR   GO; GO:0005198; F:structural molecule activity; IEA.
DR   InterPro; IPR006664; Bac_OmpA.
DR   InterPro; IPR001035; MotY.
DR   InterPro; IPR002368; OmpA.
DR   InterPro; IPR006665; OmpA/MotB.
DR   InterPro; IPR006690; OMPA_LIKE.
DR   InterPro; IPR000498; OmpA_tmem.
DR   Pfam; PF00691; OmpA; 1.
DR   Pfam; PF01389; OmpA_membrane; 1.
DR   PRINTS; PR01023; NAFLGMOTY.
DR   PRINTS; PR01021; OMPADOMAIN.
DR   PRINTS; PR01022; OUTRMMBRANEA.
DR   ProDom; PD000930; OmpA/MotB; 1.
DR   PROSITE; PS01068; OMPA; 1.
KW   Complete proteome.
SQ   SEQUENCE   350 AA;  37477 MW;  EEB90059DFCADFD3 CRC64;

  Query Match             82.2%;  Score 1499;  DB 2;  Length 350;
  Best Local Similarity   82.8%;  Pred. No. 6e-107;
  Matches  279;  Conservative   26;  Mismatches   26;  Indels    6;  Gaps    2;

Qy          6 VLNAAPKDNTWYAGGKLGWSQYHDTGFYGNGFQNNNGPTRNDQLGAGAFGGYQVNPYLGF 65
              |  |||||||||| ||||||||||      :|:|||  :||||||||||||||:||
Db         18 VAQAAPKDNTWYAGAKLGWSQYHDTGFI-----HNDGPTHENQLGAGAFGGYQVNPYVGF 72

Qy         66 EMGYDWLGRMAYKGSVDNGAFKAQGVQLTAKLGYPITDDLDIYTRLGGMVWRADSKGNYA 125
              |||||||||| |||   |||:||||||||||||||||||:||||||||||||:| |
Db         73 EMGYDWLGRMPYKGDNTNGAYKAQGVQLTAKLGYPITDDLDVYTRLGGMVWRADTKSNVP 132

Qy        126 STGVSRSEHDTGVSPVFAGGVEWAVTRDIATRLEYQWVNNIGDAGTVGTRPDNGMLSLGV 185
                | |  :|||||||||||:|:|:| :|||||||| |||||| |:||||||:||:||
Db        133 G-GASTKDHDTGVSPVFAGGIEYAITPEIATRLEYQWTNNIGDANTIGTRPDNGLLSVGV 191

Qy        186 SYRFGQEDAAPVVAPAPAPAPEVATKHFTLKSDVLFNFNKATLKPEGQQALDQLYTQLSN 245
              ||||||::|||||||||||||| ||||||||||||||||:|||||||||||:||||
Db        192 SYRFGQQEAAPVVAPAPAPAPEVQTKHFTLKSDVLFNFNKSTLKPEGQQALDQLYSQLSN 251

Qy        246 MDPKDGSAVVLGYTDRIGSEAYNQQLSEKRAQSVVDYLVAKGIPAGKISARGMGESNPVT 305
              :|||||| ||||:|||||||:|||| ||||||||||||::|||||: ||||||||||||||
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Db        252 LDPKDGSVVVLGFTDRIGSDAYNQGLSEKRAQSVVDYLISKGIPSDKISARGMGESNPVT 311

Qy        306 GNTCDNVKARAALIDCLAPDRRVEIEVKGYKEVVTQP 342
              |||||||| |||||||||||||||||||| |:|||||
Db        312 GNTCDNVKPRAALIDCLAPDRRVEIEVKGVKDVVTQP 348


RESULT 11
OMPA_SALTY
ID   OMPA_SALTY     STANDARD;      PRT;   350 AA.
AC   P02936;
DT   21-JUL-1986 (Rel. 01, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Outer membrane protein A precursor (Outer membrane protein 33K) (Outer
DE   membrane major heat-modifiable protein).
GN   Name=ompA; OrderedLocusNames=STM1070;
OS   Salmonella typhimurium.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC   Enterobacteriaceae; Salmonella.
OX   NCBI_TaxID=602;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=83287368; PubMed=6349993;
RA   Freudl R., Cole S.T.;
RT   "Cloning and molecular characterization of the ompA gene from
RT   Salmonella typhimurium.";
RL   Eur. J. Biochem. 134:497-502(1983).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=LT2 / SGSC1412 / ATCC 700720;
RX   MEDLINE=21534948; PubMed=11677609; DOI=10.1038/35101614;
RA   McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA   Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
RA   Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA   Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
RA   Waterston R., Wilson R.K.;
RT   "Complete genome sequence of Salmonella enterica serovar Typhimurium
RT   LT2.";
RL   Nature 413:852-856(2001).
CC   -!- FUNCTION: Required for the action of colicins K and L and for the
CC       stabilization of mating aggregates in conjugation. Serves as a
CC       receptor for a number of T-even like phages. Also acts as a porin
CC       with low permeability that allows slow penetration of small
CC       solutes (By similarity).
CC   -!- SUBUNIT: Monomer (Probable).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane.
CC   -!- SIMILARITY: Belongs to the ompA family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X02006; CAA26037.1; -.
DR   EMBL; AE008746; AAL20003.1; -.
DR   PIR; A03436; MMEBAT.
DR   HSSP; P02934; 1QJP.
DR   StyGene; SG10263; ompA.
DR   InterPro; IPR006664; Bac_OmpA.
DR   InterPro; IPR002368; OmpA.
DR   InterPro; IPR006665; OmpA/MotB.
DR   InterPro; IPR006690; OMPA_LIKE.
DR   InterPro; IPR000498; OmpA_tmem.
DR   Pfam; PF00691; OmpA; 1.
DR   Pfam; PF01389; OmpA_membrane; 1.
DR   PRINTS; PR01021; OMPADOMAIN.
DR   ProDom; PD000930; OmpA/MotB; 1.
DR   PROSITE; PS01068; OMPA; 1.
KW   Complete proteome; Conjugation; Outer membrane; Phage recognition;
KW   Porin; Repeat; Signal; Transmembrane.
FT   SIGNAL       1     21
FT   CHAIN       22    350       Outer membrane protein A.
FT   TRANSMEM     27     40       Potential.
FT   TRANSMEM     55     67       Potential.
FT   TRANSMEM     70     85       Potential.
FT   TRANSMEM     97    107       Potential.
FT   TRANSMEM    111    126       Potential.
FT   TRANSMEM    146    157       Potential.
FT   TRANSMEM    163    179       Potential.
FT   TRANSMEM    185    196       Potential.
FT   DOMAIN      205    212       4 X 2 AA tandem repeats of A-P.
FT   REPEAT      205    206       1.
FT   REPEAT      207    208       2.
FT   REPEAT      209    210       3.
FT   REPEAT      211    212       4.
FT   DOMAIN      261    305       OmpA-like.
FT   DISULFID    315    327       By similarity.
FT   CONFLICT    114    114       V -> F (in Ref. 1).
FT   CONFLICT    247    247       S -> I (in Ref. 1).
SQ   SEQUENCE   350 AA;  37515 MW;  B4AC52C8C5DF54FE CRC64;

  Query Match             82.0%;  Score 1495;  DB 1;  Length 350;
  Best Local Similarity   82.8%;  Pred. No. 1.2e-106;
  Matches  279;  Conservative   26;  Mismatches   26;  Indels    6;  Gaps    2;

Qy          6 VLNAAPKDNTWYAGGKLGWSQYHDTGFYGNGFQNNNGPTRNDQLGAGAFGGYQVNPYLGF 65
              | |||||||||||| ||||||||||||      :|:|||  :||||||||||||||:||
Db         18 VAQAAPKDNTWYAGAKLGWSQYHDTGFI-----HNDGPTHENQLGAGAFGGYQVNPYVGF 72

Qy         66 EMGYDWLGRMAYKGSVDNGAFKAQGVQLTAKLGYPITDDLDIYTRLGGMVWRADSKGNYA 125
              |||||||||| |||   |||:||||||||||||||||||:||||||||||:| |
Db         73 EMGYDWLGRMPYKGDNINGAYKAQGVQLTAKLGYPITDDLDVYTRLGGMVWRADTKSNVP 132

Qy        126 STGVSRSEHDTGVSPVFAGGVEWAVTRDIATRLEYQWVNNIGDAGTVGTRPDNGMLSLGV 185
               | |  :|||||||||||:|:|:| :|||||||| |||||| |:||||||:||:||
Db        133 G-GPSTKDHDTGVSPVFAGGIEYAITPEIATRLEYQWTNNIGDANTIGTRPDNGLLSVGV 191

Qy        186 SYRFGQEDAAPVVAPAPAPAPEVATKHFTLKSDVLFNFNKATLKPEGQQALDQLYTQLSN 245
              ||||||::|||||||||||||| ||||||||||||||:|||||||||||||:||||
Db        192 SYRFGQQEAAPVVAPAPAPAPEVQTKHFTLKSDVLFNFNKSTLKPEGQQALDQLYSQLSN 251

Qy        246 MDPKDGSAVVLGYTDRIGSEAYNQQLSEKRAQSVVDYLVAKGIPAGKISARGMGESNPVT 305
              :|||||| ||||:||||||:|||| |||||||||||::||||: ||||||||||||
Db        252 LDPKDGSVVVLGFTDRIGSDAYNQGLSEKRAQSVVDYLISKGIPSDKISARGMGESNPVT 311

Qy        306 GNTCDNVKARAALIDCLAPDRRVEIEVKGYKEVVTQP 342
              |||||||| |||||||||||||||||||| |:|||||
Db        312 GNTCDNVKPRAALIDCLAPDRRVEIEVKGVKDVVTQP 348


RESULT 12
Q8CW76
ID   Q8CW76      PRELIMINARY;      PRT;   379 AA.
AC   Q8CW76;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Outer membrane protein A.
GN   Name=ompA; OrderedLocusNames=c1093;
OS   Escherichia coli O6.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC   Enterobacteriaceae; Escherichia.
OX   NCBI_TaxID=217992;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=O6:H1 / CFT073 / ATCC 700928 / UPEC;
RX   MEDLINE=22388234; PubMed=12471157;
RA   Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
RA   Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
RA   Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
RA   Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
RT   "Extensive mosaic structure revealed by the complete genome sequence
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RT   of uropathogenic Escherichia coli.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
CC   -!- SIMILARITY: Belongs to the ompA family.
DR   EMBL; AE016758; AAN79561.1; -.
DR   HSSP; P02934; 1QJP.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0009279; C:outer membrane (sensu Gram-negative Bacteria); IEA.
DR   GO; GO:0005198; F:structural molecule activity; IEA.
DR   InterPro; IPR006664; Bac_OmpA.
DR   InterPro; IPR002368; OmpA.
DR   InterPro; IPR006665; OmpA/MotB.
DR   InterPro; IPR006690; OMPA_LIKE.
DR   InterPro; IPR000498; OmpA_tmem.
DR   Pfam; PF00691; OmpA; 1.
DR   Pfam; PF01389; OmpA_membrane; 1.
DR   PRINTS; PR01021; OMPADOMAIN.
DR   PRINTS; PR01022; OUTRMMBRANEA.
DR   ProDom; PD000930; OmpA/MotB; 1.
DR   PROSITE; PS01068; OMPA; 1.
KW   Complete proteome.
SQ   SEQUENCE   379 AA;  41054 MW;  CE396D152EB1EDCA CRC64;

  Query Match             81.6%;  Score 1487;  DB 2;  Length 379;
  Best Local Similarity   83.7%;  Pred. No. 5.6e-106;
  Matches  282;  Conservative   17;  Mismatches   32;  Indels    6;  Gaps    2;

Qy          6 VLNAAPKDNTWYAGGKLGWSQYHDTGFYGNGFQNNNGPTRNDQLGAGAFGGYQVNPYLGF 65
              |  |||||||||  | ||||||||||||        |||||  :|||||||||||||||:||
Db         47 VAQAAPKDNTWYTGAKLGWSQYHDTGFI-----PNNGPTHENQLGAGAFGGYQVNPYVGF 101

Qy         66 EMGYDWLGRMAYKGSVDNGAFKAQGVQLTAKLGYPITDDLDIYTRLGGMVWRADSKGNYA 125
              ||||||||||  |||    |||:||||||||||||||||||||||||||||||||:| |
Db        102 EMGYDWLGRMPYKGDNINGAYKAQGVQLTAKLGYPITDDLDIYTRLGGMVWRADTKANVP 161

Qy        126 STGVSRSEHDTGVSPVFAGGVEWAVTRDIATRLEYQWVNNIGDAGTVGTRPDNGMLSLGV 185
                | |  :|||||||||||||||:|:| :|||||||| |||||| |:|||||||||||||
Db        162 G-GASFKDHDTGVSPVFAGGVEYAITPEIATRLEYQWTNNIGDAHTIGTRPDNGMLSLGV 220

Qy        186 SYRFGQEDAAPVVAPAPAPAPEVATKHFTLKSDVLFNFNKATLKPEGQQALDQLYTQLSN 245
              ||||||  : |||||||||||||| |||||||||||| |||||||||||:|||| ||||
Db        221 SYRFGQGEVAPVVAPAPAPAPEVQTKHFTLKSDVLFTFNKATLKPEGQAALDQLYSQLSN 280

Qy        246 MDPKDGSAVVLGYTDRIGSEAYNQQLSEKRAQSVVDYLVAKGIPAGKISARGMGESNPVT 305
              :|||||| ||||||||||:|||| |||:|||||||::||||| ||||||||||||||||
Db        281 LDPKDGSVVVLGYTDRIGSDAYNQALSERRAQSVVDYLISKGIPADKISARGMGESNPVT 340

Qy        306 GNTCDNVKARAALIDCLAPDRRVEIEVKGYKEVVTQP 342
              ||||||||  |||||||||||||||||||||  |:|||||
Db        341 GNTCDNVKQRAALIDCLAPDRRVEIEVKGIKDVVTQP 377


RESULT 13
Q7UD17
ID   Q7UD17      PRELIMINARY;      PRT;   348 AA.
AC   Q7UD17;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Outer membrane protein 3a (II*;G;d).
GN   Name=ompA; OrderedLocusNames=S1023;
OS   Shigella flexneri.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC   Enterobacteriaceae; Shigella.
OX   NCBI_TaxID=623;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=2457T;
RX   MEDLINE=22590274; PubMed=12704152;
RA   Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W.,
RA   Fournier G., Mayhew G.F., Plunkett G. III, Rose D.J., Darling A.,
RA   Mau B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S.,
RA   Schwartz D.C., Blattner F.R.;
RT   "Complete genome sequence and comparative genomics of Shigella
RT   flexneri serotype 2a strain 2457T.";
RL   Infect. Immun. 71:2775-2786(2003).
DR   EMBL; AE016981; AAP16471.1; -.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0009279; C:outer membrane (sensu Gram-negative Bacteria); IEA.
DR   InterPro; IPR006665; OmpA/MotB.
DR   InterPro; IPR006690; OMPA_LIKE.
DR   InterPro; IPR000498; OmpA_tmem.
DR   Pfam; PF00691; OmpA; 1.
DR   Pfam; PF01389; OmpA_membrane; 1.
DR   ProDom; PD000930; OmpA/MotB; 1.
DR   PROSITE; PS01068; OMPA; 1.
SQ   SEQUENCE   348 AA;  37283 MW;  42623C67041D62F4 CRC64;

  Query Match             80.8%;  Score 1473;  DB 2;  Length 348;
  Best Local Similarity   83.4%;  Pred. No. 6e-105;
  Matches  281;  Conservative   18;  Mismatches   30;  Indels    8;  Gaps    3;

Qy          6 VLNAAPKDNTWYAGGKLGWSQYHDTGFYGNGFQNNNGPTRNDQLGAGAFGGYQVNPYLGF 65
              |  |||||||||  | ||||||||||||        |||||  :|||||||||||||||:||
Db         18 VAQAAPKDNTWYTGAKLGWSQYHDTGFI-----PNNGPTHENQLGAGAFGGYQVNPYVGF 72

Qy         66 EMGYDWLGRMAYKGSVDNGAFKAQGVQLTAKLGYPITDDLDIYTRLGGMVWRADSKGNYA 125
              ||||||||||  |||    |||:||||||||||||||||||||||||||||||||:| |
Db         73 EMGYDWLGRMPYKGDNINGAYKAQGVQLTAKLGYPITDDLDIYTRLGGMVWRADTKANVP 132

Qy        126 STGVSRSEHDTGVSPVFAGGVEWAVTRDIATRLEYQWVNNIGDAGTVGTRPDNGMLSLGV 185
                | |  :|||||||||||||||:|:| :|||||||| |||||| |:|||||||||||||
Db        133 G-GASFKDHDTGVSPVFAGGVEYAITPEIATRLEYQWTNNIGDANTIGTRPDNGLLSLGV 191

Qy        186 SYRFGQEDAAPVVAPAPAPAPEVATKHFTLKSDVLFNFNKATLKPEGQQALDQLYTQLSN 245
              ||||||  : |||||||||||||| |||||||||||| |||||||||||:|||| ||||
Db        192 SYRFGQGEAAPVV--APAPAPEVQTKHFTLKSDVLFNFNKATLKPEGQAALDQLYSQLSN 249

Qy        246 MDPKDGSAVVLGYTDRIGSEAYNQQLSEKRAQSVVDYLVAKGIPAGKISARGMGESNPVT 305
              :|||||| ||||||||||:|||| |||:|||||||::||||| ||||||||||||||||
Db        250 LDPKDGSVVVLGYTDRIGSDAYNQGLSERRAQSVVDYLISKGIPADKISARGMGESNPVT 309

Qy        306 GNTCDNVKARAALIDCLAPDRRVEIEVKGYKEVVTQP 342
              ||||||||  |||||||||||||||||||||  |:|||||
Db        310 GNTCDNVKQRAALIDCLAPDRRVEIEVKGIKDVVTQP 346


RESULT 14
Q83RX2
ID   Q83RX2      PRELIMINARY;      PRT;   372 AA.
AC   Q83RX2;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Outer membrane protein A.
GN   Name=ompA; OrderedLocusNames=SF0957;
OS   Shigella flexneri.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC   Enterobacteriaceae; Shigella.
OX   NCBI_TaxID=623;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=301 / Serotype 2a;
RX   MEDLINE=22272406; PubMed=12384590;
RA   Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
RA   Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
RA   Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
RA   Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
RA   Yu J.;
RT   "Genome sequence of Shigella flexneri 2a: insights into pathogenicity
RT   through comparison with genomes of Escherichia coli K12 and O157.";
RL   Nucleic Acids Res. 30:4432-4441(2002).
CC   -!- SIMILARITY: Belongs to the ompA family.
DR   EMBL; AE015125; AAN42586.1; -.
DR   HSSP; P02934; 1QJP.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0009279; C:outer membrane (sensu Gram-negative Bacteria); IEA.
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DR   GO; GO:0005198; F:structural molecule activity; IEA.
DR   InterPro; IPR006664; Bac_OmpA.
DR   InterPro; IPR002368; OmpA.
DR   InterPro; IPR006665; OmpA/MotB.
DR   InterPro; IPR006690; OMPA_LIKE.
DR   InterPro; IPR000498; OmpA_tmem.
DR   Pfam; PF00691; OmpA; 1.
DR   Pfam; PF01389; OmpA_membrane; 1.
DR   PRINTS; PR01021; OMPADOMAIN.
DR   PRINTS; PR01022; OUTRMMBRANEA.
DR   ProDom; PD000930; OmpA/MotB; 1.
DR   PROSITE; PS01068; OMPA; 1.
KW   Complete proteome.
SQ   SEQUENCE   372 AA;  40289 MW;  E5D55235E1F0CF1B CRC64;

  Query Match             80.8%;  Score 1473;  DB 2;  Length 372;
  Best Local Similarity   83.4%;  Pred. No. 6.5e-105;
  Matches  281;  Conservative   18;  Mismatches   30;  Indels    8;  Gaps    3;

Qy          6 VLNAAPKDNTWYAGGKLGWSQYHDTGFYGNGFQNNNGPTRNDQLGAGAFGGYQVNPYLGF 65
              |  |||||||| | ||||||||||       |||||  :||||||||||||||:||
Db         42 VAQAAPKDNTWYTGAKLGWSQYHDTGFI-----PNNGPTHENQLGAGAFGGYQVNPYVGF 96

Qy         66 EMGYDWLGRMAYKGSVDNGAFKAQGVQLTAKLGYPITDDLDIYTRLGGMVWRADSKGNYA 125
              ||||||||||  |||   |||:||||||||||||||||||||||||||||:| |
Db         97 EMGYDWLGRMPYKGDNINGAYKAQGVQLTAKLGYPITDDLDIYTRLGGMVWRADTKANVP 156

Qy        126 STGVSRSEHDTGVSPVFAGGVEWAVTRDIATRLEYQWVNNIGDAGTVGTRPDNGMLSLGV 185
                | |  :|||||||||||||:|:| :||||||| |||||| |:|||||:|||||
Db        157 G-GASFKDHDTGVSPVFAGGVEYAITPEIATRLEYQWTNNIGDANTIGTRPDNGLLSLGV 215

Qy        186 SYRFGQEDAAPVVAPAPAPAPEVATKHFTLKSDVLFNFNKATLKPEGQQALDQLYTQLSN 245
              |||||| :|||||  |||||||| |||||||||||||||||||||| ||||||:||||
Db        216 SYRFGQGEAAPVV--APAPAPEVQTKHFTLKSDVLFNFNKATLKPEGQAALDQLYSQLSN 273

Qy        246 MDPKDGSAVVLGYTDRIGSEAYNQQLSEKRAQSVVDYLVAKGIPAGKISARGMGESNPVT 305
              :|||||| |||||||||||:|||| |||:|||||||::||||| ||||||||||||||
Db        274 LDPKDGSVVVLGYTDRIGSDAYNQGLSERRAQSVVDYLISKGIPADKISARGMGESNPVT 333

Qy        306 GNTCDNVKARAALIDCLAPDRRVEIEVKGYKEVVTQP 342
              |||||||| |||||||||||||||||| |:|||||
Db        334 GNTCDNVKQRAALIDCLAPDRRVEIEVKGIKDVVTQP 370


RESULT 15
Q7X0I7
ID   Q7X0I7      PRELIMINARY;      PRT;   327 AA.
AC   Q7X0I7;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Outer membrane protein A (Fragment).
GN   Name=ompA;
OS   Shigella flexneri 2a.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC   Enterobacteriaceae; Shigella.
OX   NCBI_TaxID=42897;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=USM480;
RA   Mohd Zaki S., Kirnpal-Kaur B., Ravichandran M., Asma I.;
RL   Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Belongs to the ompA family.
DR   EMBL; AY305875; AAP74760.2; -.
DR   GO; GO:0009288; C:flagellum (sensu Bacteria); IEA.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0009279; C:outer membrane (sensu Gram-negative Bacteria); IEA.
DR   GO; GO:0003774; F:motor activity; IEA.
DR   GO; GO:0005198; F:structural molecule activity; IEA.
DR   GO; GO:0001539; P:ciliary/flagellar motility; IEA.
DR   InterPro; IPR006664; Bac_OmpA.
DR   InterPro; IPR001035; MotY.
DR   InterPro; IPR002368; OmpA.
DR   InterPro; IPR006665; OmpA/MotB.
DR   InterPro; IPR006690; OMPA_LIKE.
DR   InterPro; IPR000498; OmpA_tmem.
DR   Pfam; PF00691; OmpA; 1.
DR   Pfam; PF01389; OmpA_membrane; 1.
DR   PRINTS; PR01023; NAFLGMOTY.
DR   PRINTS; PR01021; OMPADOMAIN.
DR   PRINTS; PR01022; OUTRMMBRANEA.
DR   ProDom; PD000930; OmpA/MotB; 1.
DR   PROSITE; PS01068; OMPA; 1.
FT   NON_TER       1       1
SQ   SEQUENCE   327 AA;  35254 MW;  31AEFD69EF7A6182 CRC64;

  Query Match             80.4%;  Score 1466;  DB 2;  Length 327;
  Best Local Similarity   83.8%;  Pred. No. 1.9e-104;
  Matches  279;  Conservative   18;  Mismatches   28;  Indels    8;  Gaps    3;

Qy         10 APKDNTWYAGGKLGWSQYHDTGFYGNGFQNNNGPTRNDQLGAGAFGGYQVNPYLGFEMGY 69
              ||||||| | ||||||||||       |||||  :|||||||||||||:||||||
Db          1 APKDNTWYTGAKLGWSQYHDTGFI-----PNNGPTHENQLGAGAFGGYQVNPYVGFEMGY 55

Qy         70 DWLGRMAYKGSVDNGAFKAQGVQLTAKLGYPITDDLDIYTRLGGMVWRADSKGNYASTGV 129
              |||||| |||   |||:||||||||||||||||||||||||||||:| |    |
Db         56 DWLGRMPYKGDNINGAYKAQGVQLTAKLGYPITDDLDIYTRLGGMVWRADTKANVPG-GA 114

Qy        130 SRSEHDTGVSPVFAGGVEWAVTRDIATRLEYQWVNNIGDAGTVGTRPDNGMLSLGVSYRF 189
              |  :|||||||||||:|:| :||||||| |||||| |:|||||:|||||||||
Db        115 SFKDHDTGVSPVFAGGVEYAITPEIATRLEYQWTNNIGDANTIGTRPDNGLLSLGVSYRF 174

Qy        190 GQEDAAPVVAPAPAPAPEVATKHFTLKSDVLFNFNKATLKPEGQQALDQLYTQLSNMDPK 249
              || :|||||  |||||||| |||||||||||||||||||||| ||||||:||||:|||
Db        175 GQGEAAPVV--APAPAPEVQTKHFTLKSDVLFNFNKATLKPEGQAALDQLYSQLSNLDPK 232

Qy        250 DGSAVVLGYTDRIGSEAYNQQLSEKRAQSVVDYLVAKGIPAGKISARGMGESNPVTGNTC 309
              ||| |||||||||:|||| |||:|||||||::||||| ||||||||||||||||
Db        233 DGSVVVLGYTDRIGSDAYNQGLSERRAQSVVDYLISKGIPADKISARGMGESNPVTGNTC 292

Qy        310 DNVKARAALIDCLAPDRRVEIEVKGYKEVVTQP 342
              |||| |||||||||||||||||| |:|||||
Db        293 DNVKQRAALIDCLAPDRRVEIEVKGIKDVVTQP 325


Search completed: January 19, 2005, 18:16:30
Job time : 100 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: January 19, 2005, 17:58:00 ; Search time 24 Seconds
(without alignments)
1379.107 Million cell updates/sec

Title: US-09-913-772-2
Perfect score: 1823
Sequence: 1 MKAIFVLNAAPKDNTWYAGG.....DRRVEIEVKGYKEVVTQPAG 344

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1782	97.8	356	2	JC6558	outer membrane pro
2	1542	84.6	350	2	S07222	outer membrane pro
3	1525.5	83.7	351	1	MMEBAD	outer membrane pro
4	1511	82.9	346	1	MMECA	outer membrane pro
5	1511	82.9	346	2	A90759	outer membrane pro
6	1511	82.9	346	2	G85622	outer membrane pro
7	1499	82.2	350	2	AI0626	outer membrane pro
8	1490	81.7	350	1	MMEBAT	outer membrane pro
9	1381.5	75.8	359	2	S07298	outer membrane pro
10	1325.5	72.7	353	2	AD0175	probable outer mem
11	1128.5	61.9	238	2	I62385	outer membrane pro
12	1112.5	61.0	244	2	I62393	outer membrane pro
13	1111	60.9	243	2	I62388	outer membrane pro
14	1110.5	60.9	244	2	I62389	outer membrane pro
15	1109	60.8	243	2	I84531	outer membrane pro
16	1106	60.7	243	2	I62386	outer membrane pro
17	1089	59.7	241	2	I62387	outer membrane pro
18	1084	59.5	241	2	I62391	outer membrane pro
19	1074.5	58.9	240	2	I62394	outer membrane pro
20	1056.5	58.0	238	2	I40703	outer membrane pro
21	646.5	35.5	353	2	C64187	outer membrane pro
22	515	28.3	349	2	E84968	outer membrane pro
23	443.5	24.3	321	2	F82104	outer membrane pro
24	271	14.9	194	2	A45275	21K outer membrane
25	262	14.4	236	2	A27894	outer membrane pro
26	255	14.0	242	2	C81205	outer membrane pro
27	251	13.8	240	2	A37004	outer membrane cla
28	250	13.7	242	2	A81782	outer membrane pro
29	243	13.3	326	2	S20494	root adhesin - Pse
30	231.5	12.7	350	2	S39156	outer membrane pro
31	227.5	12.5	407	2	H87341	OmpA family protei
32	208.5	11.4	319	2	C81294	outer membrane fib
33	206	11.3	344	2	A39139	outer membrane pro
34	206	11.3	389	2	B82819	outer membrane pro
35	199	10.9	210	2	A83516	probable outer mem
36	193.5	10.6	449	2	D87682	OmpA family protei
37	179	9.8	219	2	S47773	hypothetical 22.2K
38	176.5	9.7	261	2	E83185	probable outer mem
39	176	9.7	220	2	AC0982	probable outer mem
40	174	9.5	219	2	E91183	probable outer mem
41	174	9.5	219	2	A86030	probable outer mem
42	173.5	9.5	326	2	H70782	probable ompA prot
43	171.5	9.4	420	2	H95302	probable membrane
44	170	9.3	223	2	C82230	probable lipoprote
45	169.5	9.3	237	2	A83541	hypothetical prote

ALIGNMENTS

RESULT 1
JC6558
outer membrane protein A precursor - Klebsiella pneumoniae
C;Species: Klebsiella pneumoniae
C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 07-May-1999
C;Accession: JC6558
R;Nguyen, T.N.; Samuelson, P.; Sterky, F.; Merle-Poitte, C.; Robert, A.; Baussant, T.; H
Gene 210, 93-101, 1998
A;Title: Chromosomal sequencing using a PCR-based biotin-capture method allowed isolatio
A;Reference number: JC6558; MUID:98192544; PMID:9524233
A;Accession: JC6558
A;Molecule type: DNA
A;Residues: 1-356 <NGU>
A;Experimental source: IP I145
C;Genetics:
A;Gene: ompA
C;Superfamily: outer membrane protein A
C;Keywords: membrane protein
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-356/Product: outer membrane protein A #status predicted <MAT>

Query Match 97.8%; Score 1782; DB 2; Length 356;
Best Local Similarity 99.4%; Pred. No. 4.1e-127;
Matches 336; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy          6 VLNAAPKDNTWYAGGKLGWSQYHDTGFYGNGFQNNNGPTRNDQLGAGAFGGYQVNPYLGF 65
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Db         18 VAQAAPKDNTWYAGGKLGWSQYHDTGFYGNGFQNNNGPTRNDQLGAGAFGGYQVNPYLGF 77

Qy         66 EMGYDWLGRMAYKGSVDNGAFKAQGVQLTAKLGYPITDDLDIYTRLGGMVWRADSKGNYA 125
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         78 EMGYDWLGRMAYKGSVDNGAFKAQGVQLTAKLGYPITDDLDIYTRLGGMVWRADSKGNYA 137

Qy        126 STGVSRSEHDTGVSPVFAGGVEWAVTRDIATRLEYQWVNNIGDAGTVGTRPDNGMLSLGV 185
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        138 STGVSRSEHDTGVSPVFAGGVEWAVTRDIATRLEYQWVNNIGDAGTVGTRPDNGMLSLGV 197

Qy        186 SYRFGQEDAAPVVAPAPAPAPEVATKHFTLKSDVLFNFNKATLKPEGQQALDQLYTQLSN 245
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        198 SYRFGQEDAAPVVAPAPAPAPEVATKHFTLKSDVLFNFNKATLKPEGQQALDQLYTQLSN 257

Qy        246 MDPKDGSAVVLGYTDRIGSEAYNQQLSEKRAQSVVDYLVAKGIPAGKISARGMGESNPVT 305
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        258 MDPKDGSAVVLGYTDRIGSEAYNQQLSEKRAQSVVDYLVAKGIPAGKISARGMGESNPVT 317

Qy        306 GNTCDNVKARAALIDCLAPDRRVEIEVKGYKEVVTQPA 343
              |||||||||||||||||||||||||||||||||||||
Db        318 GNTCDNVKARAALIDCLAPDRRVEIEVKGYKEVVTQPA 355
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RESULT 2
S07222

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outer membrane protein ompA precursor - Enterobacter aerogenes
C;Species: Enterobacter aerogenes
C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 09-Jul-2004
C;Accession: S07222
R;Braun, G.; Cole, S.T.
Eur. J. Biochem. 137, 495-500, 1983
A;Title: Molecular characterization of the gene coding for major outer membrane protein
A;Reference number: S07222; MUID:84108348; PMID:6363059
A;Accession: S07222
A;Molecule type: DNA
A;Residues: 1-350 <BRA>
A;Cross-references: UNIPROT:P09146; EMBL:X00254; NID:g40837; PIDN:CAA25062.1; PID:g40838
A;Note: the authors translated the codon CAG for residue 197 as Asn
C;Genetics:
A;Gene: ompA
C;Superfamily: outer membrane protein A
C;Keywords: membrane protein
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-350/Product: outer membrane protein ompA #status predicted <MAT>
F;201-212/Region: alanine/proline-rich
F;213-350/Domain: periplasmic #status predicted <PER>

  Query Match             84.6%;  Score 1542;  DB 2;  Length 350;
  Best Local Similarity   87.5%;  Pred. No. 5.4e-109;
  Matches  295;  Conservative   10;  Mismatches   26;  Indels    6;  Gaps    2;

Qy          6 VLNAAPKDNTWYAGGKLGWSQYHDTGFYGNGFQNNNGPTRNDQLGAGAFGGYQVNPYLGF 65
              |  ||||||||||||||||||:||||:| |   ||||||   |||||||||||||||||||
Db         18 VAQAAPKDNTWYAGGKLGWSQFHDTGWY-NSNLNNNGPTHESQLGAGAFGGYQVNPYLGF 76

Qy         66 EMGYDWLGRMAYKGSVDNGAFKAQGVQLTAKLGYPITDDLDIYTRLGGMVWRADSKGNYA 125
              ||||||||| |||   |||| :| ||||||||||||||||||||||||||||||||||||
Db         77 EMGYDWLGRMPYKGVKVNGAFSSQAVQLTAKLGYPITDDLDIYTRLGGMVWRADS----- 131

Qy        126 STGVSRSEHDTGVSPVFAGGVEWAVTRDIATRLEYQWVNNIGDAGTVGTRPDNGMLSLGV 185
              |  ::   |||||||||||||||:|||||||||||||||||||||||| ||||||||:||
Db        132 SNSIAGDNHDTGVSPVFAGGVEWAMTRDIATRLEYQWVNNIGDAGTVGVRPDNGMLSVGV 191

Qy        186 SYRFGQEDAAPVVAPAPAPAPEVATKHFTLKSDVLFNFNKATLKPEGQQALDQLYTQLSN 245
              |||||||| |||||||||||||| || ||||||||||||||||||||||||||||||||||
Db        192 SYRFGQEDNAPVVAPAPAPAPEVTTKTFTLKSDVLFNFNKATLKPEGQQALDQLYTQLSN 251

Qy        246 MDPKDGSAVVLGYTDRIGSEAYNQQLSEKRAQSVVDYLVAKGIPAGKISARGMGESNPVT 305
              |||||||||||||||||| |||:|||||||||||||||||| ||||||||||:|||
Db        252 MDPKDGSAVVLGYTDRIGSEQYNQKLSEKRAQSVVDYLVAKGIPANKISARGMGESDPVT 311

Qy        306 GNTCDNVKARAALIDCLAPDRRVEIEVKGYKEVVTQP 342
              |||||||||||||||||||| |||||||:|||||
Db        312 GNTCDNVKARAALIDCLAPDRRVAIEVKGYKDVVTQP 348


RESULT 3
MMEBAD
outer membrane protein A precursor - Shigella dysenteriae
C;Species: Shigella dysenteriae
C;Date: 18-Aug-1982 #sequence_revision 18-Aug-1982 #text_change 09-Jul-2004
C;Accession: A03435
R;Braun, G.; Cole, S.T.
Nucleic Acids Res. 10, 2367-2378, 1982
A;Title: The nucleotide sequence coding for major outer membrane protein OmpA of Shigell
A;Reference number: A03435; MUID:82221414; PMID:6283478
A;Accession: A03435
A;Molecule type: DNA
A;Residues: 1-351 <BRA>
A;Cross-references: UNIPROT:P02935; GB:V01344; NID:g46943; PIDN:CAA24638.1; PID:g46945
C;Genetics:
A;Gene: ompA
C;Superfamily: outer membrane protein A
C;Keywords: transmembrane protein
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-351/Product: outer membrane protein A #status predicted <MAT>
F;22-201/Domain: intramembrane #status predicted <INT>
F;201-213/Region: alanine/proline-rich
F;214-351/Domain: periplasmic #status predicted <PER>

  Query Match             83.7%;  Score 1525.5;  DB 1;  Length 351;
  Best Local Similarity   84.6%;  Pred. No. 9.5e-108;
  Matches  285;  Conservative   20;  Mismatches   27;  Indels    5;  Gaps    1;

Qy          6 VLNAAPKDNTWYAGGKLGWSQYHDTGFYGNGFQNNNGPTRNDQLGAGAFGGYQVNPYLGF 65
              |  ||||||||| | ||||||||||||      :|||||  :||||||||||||||:||
Db         18 VAQAAPKDNTWYTGAKLGWSQYHDTGFI-----DNNGPTHENQLGAGAFGGYQVNPYVGF 72

Qy         66 EMGYDWLGRMAYKGSVDNGAFKAQGVQLTAKLGYPITDDLDIYTRLGGMVWRADSKGNYA 125
              |||||||||| |||||:|||:|||||||||||||||||||:||||||||||:| :
Db         73 EMGYDWLGRMPYKGSVENGAYKAQGVQLTAKLGYPITDDLDVYTRLGGMVWRADTKAHNN 132

Qy        126 STGVSRSEHDTGVSPVFAGGVEWAVTRDIATRLEYQWVNNIGDAGTVGTRPDNGMLSLGV 185
               || |   |||||||||||||||:| :||||||||| |||||| |:|||||||:|||||
Db        133 VTGESEKNHDTGVSPVFAGGVEWAITPEIATRLEYQWTNNIGDAHTIGTRPDNGLLSLGV 192

Qy        186 SYRFGQEDAAPVVAPAPAPAPEVATKHFTLKSDVLFNFNKATLKPEGQQALDQLYTQLSN 245
              |||||| :|||||||||||||| ||||||||||||||||||||||| ||||||:||||
Db        193 SYRFGQGEAAPVVAPAPAPAPEVQTKHFTLKSDVLFNFNKATLKPEGQAALDQLYSQLSN 252

Qy        246 MDPKDGSAVVLGYTDRIGSEAYNQQLSEKRAQSVVDYLVAKGIPAGKISARGMGESNPVT 305
              :|||||| ||||||||||:|||| |||:|||||||::||||| ||||||||||||||
Db        253 LDPKDGSVVVLGYTDRIGSDAYNQGLSERRAQSVVDYLISKGIPADKISARGMGESNPVT 312

Qy        306 GNTCDNVKARAALIDCLAPDRRVEIEVKGYKEVVTQP 342
              |||||||| |||||||||||||||||||| |:|||||
Db        313 GNTCDNVKQRAALIDCLAPDRRVEIEVKGIKDVVTQP 349


RESULT 4
MMECA
outer membrane protein A precursor - Escherichia coli (strain K-12)
N;Alternate names: outer membrane protein II*
C;Species: Escherichia coli
C;Date: 30-Sep-1980 #sequence_revision 30-Sep-1980 #text_change 09-Jul-2004
C;Accession: A93707; A92862; A93855; S50909; D64836; A03434
R;Beck, E.; Bremer, E.
Nucleic Acids Res. 8, 3011-3024, 1980
A;Title: Nucleotide sequence of the gene ompA coding the outer membrane protein II of Esc
A;Reference number: A93707; MUID:81053729; PMID:6253901
A;Accession: A93707
A;Molecule type: DNA
A;Residues: 1-346 <BEC>
A;Cross-references: UNIPROT:P02934; GB:V00307; GB:J01654; NID:g42159; PIDN:CAA23588.1; PI
A;Experimental source: strain K12
R;Movva, N.R.; Nakamura, K.; Inouye, M.
J. Mol. Biol. 143, 317-328, 1980
A;Title: Gene structure of the OmpA protein, a major surface protein of Escherichia coli
A;Reference number: A92862; MUID:81170587; PMID:6260961
A;Accession: A92862
A;Molecule type: DNA
A;Residues: 1-346 <MOV>
A;Cross-references: GB:J01654; GB:V00307; GB:V00358; NID:g146979; PIDN:AAA24231.1; PID:g1
A;Experimental source: K12, strain K802
R;Chen, R.; Schmidmayr, W.; Kramer, C.; Chen-Schmeisser, U.; Henning, U.
Proc. Natl. Acad. Sci. U.S.A. 77, 4592-4596, 1980
A;Title: Primary structure of major outer membrane protein II* (ompA protein) of Escheric
A;Reference number: A93855; MUID:81054820; PMID:7001461
A;Accession: A93855
A;Molecule type: protein
A;Residues: 22-346 <CHE>
A;Experimental source: K12, strain P400
R;Kuhn, A.; Kiefer, D.; Koehne, C.; Zhu, H.Y.; Tschantz, W.R.; Dalbey, R.E.
Eur. J. Biochem. 226, 891-897, 1994
A;Title: Evidence for a loop-like insertion mechanism of pro-Omp A into the inner membrar
A;Reference number: S50909; MUID:95112855; PMID:7813480
A;Accession: S50909
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-46 <KUH>
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Col
```

.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: D64836
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-346 <BLAT>
A;Cross-references: GB:AE000198; GB:U00096; NID:g1787189; PIDN:AAC74043.1; PID:g1787191;
A;Experimental source: strain K-12, substrain MG1655
C;Genetics:
A;Gene: ompA; tolG; tut; con
A;Map position: 22 min
C;Function:
A;Description: required for the action of colicins K and L and for the stabilization of diffusion channels that allow penetration of various solutes
C;Superfamily: outer membrane protein A
C;Keywords: membrane protein; monomer
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-346/Product: outer membrane protein A #status predicted <MAT>
F;22-196/Domain: intramembrane #status predicted <INT>
F;196-208/Region: alanine/proline-rich
F;209-346/Domain: periplasmic #status predicted <PER>
F;257-301/Domain: ompA-like domain #status predicted <OMP>

Query Match 82.9%; Score 1511; DB 1; Length 346;
Best Local Similarity 84.9%; Pred. No. 1.2e-106;
Matches 286; Conservative 17; Mismatches 24; Indels 10; Gaps 2;

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Qy          6 VLNAAPKDNTWYAGGKLGWSQYHDTGFYGNGFQNNNGPTRNDQLGAGAFGGYQVNPYLGF 65
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Db         18 VAQAAPKDNTWYTGAKLGWSQYHDTGFI-----NNNGPTHENQLGAGAFGGYQVNPYVGF 72

Qy         66 EMGYDWLGRMAYKGSVDNGAFKAQGVQLTAKLGYPITDDLDIYTRLGGMVWRADSKGNYA 125
              ||||||||||  |||||:|||:|||||||||||||||||||||||||||||||||:| |
Db         73 EMGYDWLGRMPYKGSVENGAYKAQGVQLTAKLGYPITDDLDIYTRLGGMVWRADTKSN-- 130

Qy        126 STGVSRSEHDTGVSPVFAGGVEWAVTRDIATRLEYQWVNNIGDAGTVGTRPDNGMLSLGV 185
                  |    ||||||||||||||:|:| :|||||||| ||||||  |:||||||||||||
Db        131 ---VYGKNHDTGVSPVFAGGVEYAITPEIATRLEYQWTNNIGDAHTIGTRPDNGMLSLGV 187

Qy        186 SYRFGQEDAAPVVAPAPAPAPEVATKHFTLKSDVLFNFNKATLKPEGQQALDQLYTQLSN 245
              ||||||  :|||||||||||||||  |||||||||||||||||||||||||  |||||:||||
Db        188 SYRFGQGEAAPVVAPAPAPAPEVQTKHFTLKSDVLFNFNKATLKPEGQAALDQLYSQLSN 247

Qy        246 MDPKDGSAVVLGYTDRIGSEAYNQQLSEKRAQSVVDYLVAKGIPAGKISARGMGESNPVT 305
              :||||||  ||||||||||:|||| |||:||||||||::|||||  ||||||||||||||
Db        248 LDPKDGSVVVLGYTDRIGSDAYNQGLSERRAQSVVDYLISKGIPADKISARGMGESNPVT 307

Qy        306 GNTCDNVKARAALIDCLAPDRRVEIEVKGYKEVVTQP 342
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Db        308 GNTCDNVKQRAALIDCLAPDRRVEIEVKGIKDVVTQP 344
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RESULT 5
A90759
outer membrane protein 3a ECs1041 [imported] - Escherichia coli (strain O157:H7, substra
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C;Accession: A90759
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genc
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: A90759
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-346 <HAY>
A;Cross-references: UNIPROT:P02934; GB:BA000007; PIDN:BAB34464.1; PID:g13360501; GSPDB:G
A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
A;Gene: ECs1041
C;Superfamily: outer membrane protein A

Query Match 82.9%; Score 1511; DB 2; Length 346;
Best Local Similarity 84.9%; Pred. No. 1.2e-106;
Matches 286; Conservative 17; Mismatches 24; Indels 10; Gaps 2;

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Qy          6 VLNAAPKDNTWYAGGKLGWSQYHDTGFYGNGFQNNNGPTRNDQLGAGAFGGYQVNPYLGF 65
              |  |||||||||  | ||||||||||||      ||||||  :|||||||||||||||:||
Db         18 VAQAAPKDNTWYTGAKLGWSQYHDTGFI-----NNNGPTHENQLGAGAFGGYQVNPYVGF 72

Qy         66 EMGYDWLGRMAYKGSVDNGAFKAQGVQLTAKLGYPITDDLDIYTRLGGMVWRADSKGNYA 125
              ||||||||||  |||||:|||:|||||||||||||||||||||||||||||||||:| |
Db         73 EMGYDWLGRMPYKGSVENGAYKAQGVQLTAKLGYPITDDLDIYTRLGGMVWRADTKSN-- 130

Qy        126 STGVSRSEHDTGVSPVFAGGVEWAVTRDIATRLEYQWVNNIGDAGTVGTRPDNGMLSLGV 185
                  |    ||||||||||||||:|:| :|||||||| ||||||  |:||||||||||||
Db        131 ---VYGKNHDTGVSPVFAGGVEYAITPEIATRLEYQWTNNIGDAHTIGTRPDNGMLSLGV 187

Qy        186 SYRFGQEDAAPVVAPAPAPAPEVATKHFTLKSDVLFNFNKATLKPEGQQALDQLYTQLSN 245
              ||||||  :|||||||||||||||  |||||||||||||||||||||||||  |||||:||||
Db        188 SYRFGQGEAAPVVAPAPAPAPEVQTKHFTLKSDVLFNFNKATLKPEGQAALDQLYSQLSN 247

Qy        246 MDPKDGSAVVLGYTDRIGSEAYNQQLSEKRAQSVVDYLVAKGIPAGKISARGMGESNPVT 305
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RESULT 6
G85622
outer membrane protein 3a [imported] - Escherichia coli (strain O157:H7, substrain EDL93
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession: G85622
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: G85622
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-346 <STO>
A;Cross-references: UNIPROT:P02934; GB:AE005174; NID:g12514142; PIDN:AAG55443.1; GSPDB:G
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: ompA
C;Superfamily: outer membrane protein A

Query Match 82.9%; Score 1511; DB 2; Length 346;
Best Local Similarity 84.9%; Pred. No. 1.2e-106;
Matches 286; Conservative 17; Mismatches 24; Indels 10; Gaps 2;

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Qy          6 VLNAAPKDNTWYAGGKLGWSQYHDTGFYGNGFQNNNGPTRNDQLGAGAFGGYQVNPYLGF 65
              |  |||||||||  | ||||||||||||      ||||||  :|||||||||||||||:||
Db         18 VAQAAPKDNTWYTGAKLGWSQYHDTGFI-----NNNGPTHENQLGAGAFGGYQVNPYVGF 72

Qy         66 EMGYDWLGRMAYKGSVDNGAFKAQGVQLTAKLGYPITDDLDIYTRLGGMVWRADSKGNYA 125
              ||||||||||  |||||:|||:|||||||||||||||||||||||||||||||||:| |
Db         73 EMGYDWLGRMPYKGSVENGAYKAQGVQLTAKLGYPITDDLDIYTRLGGMVWRADTKSN-- 130

Qy        126 STGVSRSEHDTGVSPVFAGGVEWAVTRDIATRLEYQWVNNIGDAGTVGTRPDNGMLSLGV 185
                  |    ||||||||||||||:|:| :|||||||| ||||||  |:||||||||||||
Db        131 ---VYGKNHDTGVSPVFAGGVEYAITPEIATRLEYQWTNNIGDAHTIGTRPDNGMLSLGV 187

Qy        186 SYRFGQEDAAPVVAPAPAPAPEVATKHFTLKSDVLFNFNKATLKPEGQQALDQLYTQLSN 245
              ||||||  :|||||||||||||||  |||||||||||||||||||||||||  |||||:||||
Db        188 SYRFGQGEAAPVVAPAPAPAPEVQTKHFTLKSDVLFNFNKATLKPEGQAALDQLYSQLSN 247

Qy        246 MDPKDGSAVVLGYTDRIGSEAYNQQLSEKRAQSVVDYLVAKGIPAGKISARGMGESNPVT 305
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           :|||||| |||||||||||:|||| |||:|||||||||::||||| ||||||||||||||
Db        248 LDPKDGSVVVLGYTDRIGSDAYNQGLSERRAQSVVDYLISKGIPADKISARGMGESNPVT 307

Qy        306 GNTCDNVKARAALIDCLAPDRRVEIEVKGYKEVVTQP 342
              |||||||| |||||||||||||||||||| |:|||||
Db        308 GNTCDNVKQRAALIDCLAPDRRVEIEVKGIKDVVTQP 344


RESULT 7
AI0626
outer membrane protein A STY1091 [imported] - Salmonella enterica subsp. enterica serova
C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: AI0626
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Accession: AI0626
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-350 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD08196.1; PID:g16502245; GSPDB:GN00176
C;Genetics:
A;Gene: STY1091
C;Superfamily: outer membrane protein A

  Query Match             82.2%;  Score 1499;  DB 2;  Length 350;
  Best Local Similarity   82.8%;  Pred. No. 9.5e-106;
  Matches  279;  Conservative   26;  Mismatches   26;  Indels    6;  Gaps    2;

Qy          6 VLNAAPKDNTWYAGGKLGWSQYHDTGFYGNGFQNNNGPTRNDQLGAGAFGGYQVNPYLGF 65
              |  |||||||||||| ||||||||||||      :|:|||  :||||||||||||||:||
Db         18 VAQAAPKDNTWYAGAKLGWSQYHDTGFI-----HNDGPTHENQLGAGAFGGYQVNPYVGF 72

Qy         66 EMGYDWLGRMAYKGSVDNGAFKAQGVQLTAKLGYPITDDLDIYTRLGGMVWRADSKGNYA 125
              |||||||||| |||   |||:|||||||||||||||||:||||||||||:| |
Db         73 EMGYDWLGRMPYKGDNTNGAYKAQGVQLTAKLGYPITDDLDVYTRLGGMVWRADTKSNVP 132

Qy        126 STGVSRSEHDTGVSPVFAGGVEWAVTRDIATRLEYQWVNNIGDAGTVGTRPDNGMLSLGV 185
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Qy        186 SYRFGQEDAAPVVAPAPAPAPEVATKHFTLKSDVLFNFNKATLKPEGQQALDQLYTQLSN 245
              ||||||::|||||||||||||| ||||||||||||||:|||||||||||||:||||
Db        192 SYRFGQQEAAPVVAPAPAPAPEVQTKHFTLKSDVLFNFNKSTLKPEGQQALDQLYSQLSN 251

Qy        246 MDPKDGSAVVLGYTDRIGSEAYNQQLSEKRAQSVVDYLVAKGIPAGKISARGMGESNPVT 305
              :|||||| ||||:||||||:|||| |||||||||||::||||: |||||||||||||
Db        252 LDPKDGSVVVLGFTDRIGSDAYNQGLSEKRAQSVVDYLISKGIPSDKISARGMGESNPVT 311

Qy        306 GNTCDNVKARAALIDCLAPDRRVEIEVKGYKEVVTQP 342
              |||||||| |||||||||||||||||||| |:|||||
Db        312 GNTCDNVKPRAALIDCLAPDRRVEIEVKGVKDVVTQP 348


RESULT 8
MMEBAT
outer membrane protein A precursor - Salmonella typhimurium
N;Alternate names: outer membrane major heat-modifiable protein; outer membrane protein
C;Species: Salmonella typhimurium
C;Date: 19-Feb-1984 #sequence_revision 19-Feb-1984 #text_change 09-Jul-2004
C;Accession: A03436
R;Freudl, R.; Cole, S.T.
Eur. J. Biochem. 134, 497-502, 1983
A;Title: Cloning and molecular characterization of the ompA gene from Salmonella typhimu
A;Reference number: A03436; MUID:83287368; PMID:6349993
A;Accession: A03436
A;Molecule type: DNA
A;Residues: 1-350 <FRE>
A;Cross-references: UNIPROT:P02936; GB:X02006; NID:g47798; PIDN:CAA26037.1; PID:g758341
C;Genetics:
A;Gene: ompA
A;Map position: 20 min
C;Function:
A;Description: required for the action of colicins and for the stabilization of mating ac
A;Note: cannot serve as the receptor for the ompA-specific phages K3 and TuII
C;Superfamily: outer membrane protein A
C;Keywords: transmembrane protein
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-350/Product: outer membrane protein A #status predicted <MAT>
F;22-200/Domain: intramembrane #status predicted <INT>
F;200-212/Region: alanine/proline-rich
F;213-350/Domain: periplasmic #status predicted <PER>

  Query Match             81.7%;  Score 1490;  DB 1;  Length 350;
  Best Local Similarity   82.8%;  Pred. No. 4.5e-105;
  Matches  279;  Conservative   24;  Mismatches   28;  Indels    6;  Gaps    2;

Qy          6 VLNAAPKDNTWYAGGKLGWSQYHDTGFYGNGFQNNNGPTRNDQLGAGAFGGYQVNPYLGF 65
              |  |||||||||||| ||||||||||||      :|:|||  :||||||||||||||:||
Db         18 VAQAAPKDNTWYAGAKLGWSQYHDTGFI-----HNDGPTHENQLGAGAFGGYQVNPYVGF 72

Qy         66 EMGYDWLGRMAYKGSVDNGAFKAQGVQLTAKLGYPITDDLDIYTRLGGMVWRADSKGNYA 125
              |||||||||| |||   |||:|||||||||||||||||:||||||||||:| |
Db         73 EMGYDWLGRMPYKGDNINGAYKAQGVQLTAKLGYPITDDLDFYTRLGGMVWRADTKSNVP 132

Qy        126 STGVSRSEHDTGVSPVFAGGVEWAVTRDIATRLEYQWVNNIGDAGTVGTRPDNGMLSLGV 185
                | |  :|||||||||||||:|:|:| :|||||||| |||||| |:|||||||:||:||
Db        133 G-GPSTKDHDTGVSPVFAGGIEYAITPEIATRLEYQWTNNIGDANTIGTRPDNGLLSVGV 191

Qy        186 SYRFGQEDAAPVVAPAPAPAPEVATKHFTLKSDVLFNFNKATLKPEGQQALDQLYTQLSN 245
              ||||||::|||||||||||||| ||||||||||||||:|||||||||||||:||||
Db        192 SYRFGQQEAAPVVAPAPAPAPEVQTKHFTLKSDVLFNFNKSTLKPEGQQALDQLYIQLSN 251

Qy        246 MDPKDGSAVVLGYTDRIGSEAYNQQLSEKRAQSVVDYLVAKGIPAGKISARGMGESNPVT 305
              :|||||| ||||:||||||:|||| |||||||||||::||||: |||||||||||||
Db        252 LDPKDGSVVVLGFTDRIGSDAYNQGLSEKRAQSVVDYLISKGIPSDKISARGMGESNPVT 311

Qy        306 GNTCDNVKARAALIDCLAPDRRVEIEVKGYKEVVTQP 342
              |||||||| |||||||||||||||||||| |:|||||
Db        312 GNTCDNVKPRAALIDCLAPDRRVEIEVKGVKDVVTQP 348


RESULT 9
S07298
outer membrane protein ompA precursor - Serratia marcescens
C;Species: Serratia marcescens
C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 09-Jul-2004
C;Accession: S07298
R;Braun, G.; Cole, S.T.
Mol. Gen. Genet. 195, 321-328, 1984
A;Title: DNA sequence analysis of the Serratia marcescens ompA gene: implications for the
A;Reference number: S07298; MUID:85035845; PMID:6092858
A;Accession: S07298
A;Molecule type: DNA
A;Residues: 1-359 <BRA>
A;Cross-references: UNIPROT:P04845; EMBL:X00618; NID:g47242; PIDN:CAA25254.1; PID:g75830(
C;Genetics:
A;Gene: ompA
C;Superfamily: outer membrane protein A
C;Keywords: membrane protein
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-359/Product: outer membrane protein ompA #status predicted <MAT>
F;22-209/Domain: intramembrane #status predicted <INT>
F;210-219/Region: alanine/proline-rich
F;220-359/Domain: periplasmic #status predicted <PER>

  Query Match             75.8%;  Score 1381.5;  DB 2;  Length 359;
  Best Local Similarity   78.2%;  Pred. No. 7.4e-97;
  Matches  269;  Conservative   24;  Mismatches   44;  Indels    7;  Gaps    4;
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Qy          6 VLNAAPKDNTWYAGGKLGWSQYHDTGFYGNGFQN--NNGPTRNDQLGAGAFGGYQVNPYL 63
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Db         18 VAQAAPKDNTWYTGAKLGWSQYHDTGFYGNGYQNGIGNGPTHKDQLGAGAFLGYQANQYL 77

Qy         64 GFEMGYDWLGRMAYKGSVDNGAFKAQGVQLTAKLGYPITDDLDIYTRLGGMVWRADSKGN 123
              |||:|||||||| |||||:|||||||||||| ||| ||| |||||||||||||||||| |
Db         78 GFELGYDWLGRMPYKGSVNNGAFKAQGVQLAAKLSYPIADDLDIYTRLGGMVWRADSKAN 137

Qy        124 YASTGVSRSEHDTGVSPVFAGGVEWAVTRDIATRLEYQWVNNIGDAGTVGTRPDNGMLSL 183
              |  ||   |:|||||||: | |||:|:|:|:: ||||:||:|:|||||||| |||| ||||
Db        138 YGRTGQRLSDHDTGVSPLAAVGVEYALTKNWATRLDYQFVSNIGDAGTVGARPDNTMLSL 197

Qy        184 GVSYRFGQED-AAPVVAPAPAPAPEVATKHFTLKSDVLFNFNKATLKPEGQQALDQLYTQ 242
              ||||||||:|  ||  |||||||| | || |||||||||||||:||| ||||||||||||
Db        198 GVSYRFGQDDVVAP--APAPAPAPVVETKRFTLKSDVLFNFNKSTLKAEGQQALDQLYTQ 255

Qy        243 LSNMDPKDGSAVVLGYTDRIGSEAYNQQLSEKRAQSVVDYLVAKGIPAGKISARGMGESN 302
              ||:||||||| ||||||| :||: |||:|||:||||||||||:||||: ||||||||::
Db        256 LSSMDPKDGSVVVLGYTDAVGSDQYNQKLSEQRAQSVVDYLVSKGIPSDKISARGMGEAD 315

Qy        303 PVTGNTCDNVKARA--ALIDCLAPDRRVEIEVKGYKEVVTQPAG 344
              ||||||     ||  | | |||||||||||||| |:||||| |
Db        316 AVTGNTCGYKSGRATKAQIVCLAPDRRVEIEVKGIKDVVTQPQG 359


RESULT 10
AD0175
probable outer membrane porin A protein ompA [imported] - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Accession: AD0175
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Accession: AD0175
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-353 <KUR>
A;Cross-references: UNIPROT:Q8ZG77; GB:AL590842; PIDN:CAC90263.1; PID:g15979482; GSPDB:G
C;Genetics:
A;Gene: ompA
C;Superfamily: outer membrane protein A

  Query Match             72.7%;  Score 1325.5;  DB 2;  Length 353;
  Best Local Similarity   75.2%;  Pred. No. 1.2e-92;
  Matches  255;  Conservative   28;  Mismatches   49;  Indels    7;  Gaps    4;

Qy          6 VLNAAPKDNTWYAGGKLGWSQYHDTGFYGNGFQNNNGPTRNDQLGAGAFGGYQVNPYLGF 65
              |  ||||||||| |||||||| |||      ||:|||  |||||||| ||| | ||||
Db         18 VAQAAPKDNTWYTGGKLGWSQYQDTG----SIINNDGPTHKDQLGAGAFFGYQANQYLGF 73

Qy         66 EMGYDWLGRMAYKGSVDNGAFKAQGVQLTAKLGYPITDDLDIYTRLGGMVWRADSKGNYA 125
              |||||||||| ||| ::|||||||||||| ||| ||:  |||:||||||:|||||:||::
Db         74 EMGYDWLGRMPYKGDINNGAFKAQGVQLAAKLSYPVAQDLDVYTRLGGLVWRADAKGSF- 132

Qy        126 STGVSR-SEHDTGVSPVFAGGVEWAVTRDIATRLEYQWVNNIGDAGTVGTRPDNGMLSLG 184
                |: | | |||||||: | | |:| |:: |||:||||||||||  ||| |||||:||:|
Db        133 DGGLDRASGHDTGVSPLVALGAEYAWTKNWATRMEYQWVNNIGDRETVGARPDNGLLSVG 192

Qy        185 VSYRFGQED-AAPVVAPAPAPAPEVATKHFTLKSDVLFNFNKATLKPEGQQALDQLYTQL 243
              ||||||||| |||:||| ||||| | || ||||||||| |||| ||||||||||||| ||
Db        193 VSYRFGQEDAAAPIVAPTPAPAPIVDTKRFTLKSDVLFGFNKANLKPEGQQALDQLYAQL 252

Qy        244 SNMDPKDGSAVVLGYTDRIGSEAYNQQLSEKRAQSVVDYLVAKGIPAGKISARGMGESNP 303
              |::|||||| |||||: |||| | |  ||::|| || ||||:||||| ||:||| |::||
Db        253 SSIDPKDGSVVVLGFADRIGQPAPNLALSQRRADSVRDYLVSKGIPADKITARGEGQANP 312

Qy        304 VTGNTCDNVKARAALIDCLAPDRRVEIEVKGYKEVVTQP 342
              |||||||||| |||||:||||||||||||||||||||||
Db        313 VTGNTCDNVKPRAALIECLAPDRRVEIEVKGYKEVVTQP 351


RESULT 11
I62385
outer membrane protein ompA - Escherichia vulneris (fragment)
N;Alternate names: outer membrane protein II
C;Species: Escherichia vulneris
C;Date: 04-Sep-1997 #sequence_revision 07-Nov-1997 #text_change 09-Jul-2004
C;Accession: I62385
R;Lawrence, J.G.; Ochman, H.; Hartl, D.L.
J. Gen. Microbiol. 137, 1911-1921, 1991
A;Title: Molecular and evolutionary relationships among enteric bacteria.
A;Reference number: I40701; MUID:92065252; PMID:1955870
A;Accession: I62385
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-238 <RES>
A;Cross-references: UNIPROT:Q99114; GB:M63348; NID:g146984; PIDN:AAA24233.1; PID:g146985
C;Genetics:
A;Gene: ompA
C;Superfamily: outer membrane protein A
C;Keywords: membrane protein
F;98-109/Region: alanine/proline-rich

  Query Match             61.9%;  Score 1128.5;  DB 2;  Length 238;
  Best Local Similarity   90.1%;  Pred. No. 5.6e-78;
  Matches  219;  Conservative    7;  Mismatches   12;  Indels    5;  Gaps    1;

Qy         93 LTAKLGYPITDDLDIYTRLGGMVWRADSKGNYASTGVSRSEHDTGVSPVFAGGVEWAVTR 152
              ||||||||||||||||||||||||||||||      | ::   |||||||||||||||:||
Db          1 LTAKLGYPITDDLDIYTRLGGMVWRADS-----SNSIAGDNHDTGVSPVFAGGVEWAMTR 55

Qy        153 DIATRLEYQWVNNIGDAGTVGTRPDNGMLSLGVSYRFGQEDAAPVVAPAPAPAPEVATKH 212
              |||||||||||||||||||| ||||||||:|||||||||: |||||||||||||| ||
Db         56 DIATRLEYQWVNNIGDAGTVGVRPDNGMLSVGVSYRFGQEENAPVVAPAPAPAPEVTTKT 115

Qy        213 FTLKSDVLFNFNKATLKPEGQQALDQLYTQLSNMDPKDGSAVVLGYTDRIGSEAYNQQLS 272
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:||
Db        116 FTLKSDVLFNFNKATLKPEGQQALDQLYTQLSNMDPKDGSAVVLGYTDRIGSEQYNQKLS 175

Qy        273 EKRAQSVVDYLVAKGIPAGKISARGMGESNPVTGNTCDNVKARAALIDCLAPDRRVEIEV 332
              |||||||||||||||| ||||||||||:|||||||||||||||||||||||||||| |||
Db        176 EKRAQSVVDYLVAKGIPANKISARGMGESDPVTGNTCDNVKARAALIDCLAPDRRVAIEV 235

Qy        333 KGY 335
              |||
Db        236 KGY 238


RESULT 12
I62393
outer membrane protein ompA - Escherichia vulneris (ATCC 33822) (fragment)
N;Alternate names: outer membrane protein II
C;Species: Escherichia vulneris
A;Variety: ATCC 33822
C;Date: 04-Sep-1997 #sequence_revision 07-Nov-1997 #text_change 09-Jul-2004
C;Accession: I62393
R;Lawrence, J.G.; Ochman, H.; Hartl, D.L.
J. Gen. Microbiol. 137, 1911-1921, 1991
A;Title: Molecular and evolutionary relationships among enteric bacteria.
A;Reference number: I40701; MUID:92065252; PMID:1955870
A;Accession: I62393
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-244 <RES>
A;Cross-references: UNIPROT:Q47880; GB:M63350; NID:g147000; PIDN:AAA24241.1; PID:g147001
A;Experimental source: ATCC 33822
C;Genetics:
A;Gene: ompA
C;Superfamily: outer membrane protein A
C;Keywords: membrane protein
F;104-115/Region: alanine/proline-rich
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  Query Match            61.0%;  Score 1112.5;  DB 2;  Length 244;
  Best Local Similarity  87.2%;  Pred. No. 9.3e-77;
  Matches  212;  Conservative   15;  Mismatches   15;  Indels    1;  Gaps    1;

Qy         93 LTAKLGYPITDDLDIYTRLGGMVWRADSKGNYASTGVSRSEHDTGVSPVFAGGVEWAVTR 152
              |||||||||||||||||||||||||||:|     || |  :|||||||||||||||:||
Db          1 LTAKLGYPITDDLDIYTRLGGMVWRADAKAQVPGTGASFKDHDTGVSPVFAGGVEWAMTR 60

Qy        153 DIATRLEYQWVNNIGDAGTVGTRPDNGMLSLGVSYRFG-QEDAAPVVAPAPAPAPEVATK 211
              |||||||||||||||| |:||| ||||||:|||||| ||| ||||||||||||:|:||
Db         61 DIATRLEYQWVNNIGDAKTLGTRQDNGMLSVGVSYRFGQQEDVAPVVAPAPAPAPQVSTK 120

Qy        212 HFTLKSDVLFNFNKATLKPEGQQALDQLYTQLSNMDPKDGSAVVLGYTDRIGSEAYNQQL 271
              |||||||||||||||||||||||||:|:||||:|||||| ||||:||||||:|||| |
Db        121 HFTLKSDVLFNFNKATLKPEGQQALDQMYSQLSNLDPKDGSVVVLGFTDRIGSDAYNQGL 180

Qy        272 SEKRAQSVVDYLVAKGIPAGKISARGMGESNPVTGNTCDNVKARAALIDCLAPDRRVEIE 331
              ||||||||||||::||||: |||||||||||||||||||||| ||||||||||||||
Db        181 SEKRAQSVVDYLISKGIPSNKISARGMGESNPVTGNTCDNVKARPALIDCLAPDRRVEIE 240

Qy        332 VKG 334
              |||
Db        241 VKG 243


RESULT 13
I62388
outer membrane protein A - Escherichia fergusonii (ATCC 35472) (fragment)
N;Alternate names: outer membrane protein II
C;Species: Escherichia fergusonii
A;Variety: ATCC 35472
C;Date: 04-Sep-1997 #sequence_revision 07-Nov-1997 #text_change 09-Jul-2004
C;Accession: I62388; I62392
R;Lawrence, J.G.; Ochman, H.; Hartl, D.L.
J. Gen. Microbiol. 137, 1911-1921, 1991
A;Title: Molecular and evolutionary relationships among enteric bacteria.
A;Reference number: I40701; MUID:92065252; PMID:1955870
A;Accession: I62388
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-243 <RES>
A;Cross-references: UNIPROT:P24747; GB:M63352; NID:g146990; PIDN:AAA24236.1; PID:g146991
A;Experimental source: ATCC 35471
A;Accession: I62392
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-243 <RE2>
A;Cross-references: GB:M63353; NID:g146998; PIDN:AAA24240.1; PID:g146999
A;Experimental source: ATCC 35472
C;Genetics:
A;Gene: ompA
C;Superfamily: outer membrane protein A
C;Keywords: membrane protein
F;103-114/Region: alanine/proline-rich

  Query Match            60.9%;  Score 1111;  DB 2;  Length 243;
  Best Local Similarity  87.2%;  Pred. No. 1.2e-76;
  Matches  211;  Conservative   13;  Mismatches   18;  Indels    0;  Gaps    0;

Qy         93 LTAKLGYPITDDLDIYTRLGGMVWRADSKGNYASTGVSRSEHDTGVSPVFAGGVEWAVTR 152
              |||||||||||||||||||||||||:| :   || |   ||||||||||||||:|
Db          1 LTAKLGYPITDDLDIYTRLGGMVWRADTKAHNNVTGESEKNHDTGVSPVFAGGVEWAITP 60

Qy        153 DIATRLEYQWVNNIGDAGTVGTRPDNGMLSLGVSYRFGQEDAAPVVAPAPAPAPEVATKH 212
              :|||||||| |||||| |:|||||||:|||||||||| :|||||||||||||| |||
Db         61 EIATRLEYQWTNNIGDANTIGTRPDNGLLSLGVSYRFGQGEAAPVVAPAPAPAPEVQTKH 120

Qy        213 FTLKSDVLFNFNKATLKPEGQQALDQLYTQLSNMDPKDGSAVVLGYTDRIGSEAYNQQLS 272
              |||||||||||||||||| ||||||:||||:|||||| ||||||||||:|||| ||
Db        121 FTLKSDVLFNFNKATLKPEGQAALDQLYSQLSNLDPKDGSVVVLGYTDRIGSDAYNQGLS 180

Qy        273 EKRAQSVVDYLVAKGIPAGKISARGMGESNPVTGNTCDNVKARAALIDCLAPDRRVEIEV 332
              |:||||||||::||||| |||||||||||||||||||| |||||||||||||||||||
Db        181 ERRAQSVVDYLISKGIPADKISARGMGESNPVTGNTCDNVKQRAALIDCLAPDRRVEIEV 240

Qy        333 KG 334
              ||
Db        241 KG 242


RESULT 14
I62389
outer membrane protein ompA - Escherichia vulneris (ATCC 33821) (fragment)
N;Alternate names: outer membrane protein II
C;Species: Escherichia vulneris
A;Variety: ATCC 33821
C;Date: 04-Sep-1997 #sequence_revision 07-Nov-1997 #text_change 09-Jul-2004
C;Accession: I62389
R;Lawrence, J.G.; Ochman, H.; Hartl, D.L.
J. Gen. Microbiol. 137, 1911-1921, 1991
A;Title: Molecular and evolutionary relationships among enteric bacteria.
A;Reference number: I40701; MUID:92065252; PMID:1955870
A;Accession: I62389
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-244 <RES>
A;Cross-references: UNIPROT:Q99115; GB:M63349; NID:g146992; PIDN:AAA24237.1; PID:g146993
A;Experimental source: ATCC 33821
C;Genetics:
A;Gene: ompA
C;Superfamily: outer membrane protein A
C;Keywords: membrane protein
F;104-115/Region: alanine/proline-rich

  Query Match            60.9%;  Score 1110.5;  DB 2;  Length 244;
  Best Local Similarity  86.8%;  Pred. No. 1.3e-76;
  Matches  211;  Conservative   16;  Mismatches   15;  Indels    1;  Gaps    1;

Qy         93 LTAKLGYPITDDLDIYTRLGGMVWRADSKGNYASTGVSRSEHDTGVSPVFAGGVEWAVTR 152
              |||||||||||:|||||||||||||:|     || |  :|||||||||||||||:||
Db          1 LTAKLGYPITDDVDIYTRLGGMVWRADAKSQVGGTGASFKDHDTGVSPVFAGGVEWAMTR 60

Qy        153 DIATRLEYQWVNNIGDAGTVGTRPDNGMLSLGVSYRFG-QEDAAPVVAPAPAPAPEVATK 211
              |||||||||||||||| |:||| ||||||:|||||| ||| ||||||||||:|:||
Db         61 DIATRLEYQWVNNIGDAKTLGTRQDNGMLSVGVSYRFGQQEDVAPVVAPAPAPAPQVSTK 120

Qy        212 HFTLKSDVLFNFNKATLKPEGQQALDQLYTQLSNMDPKDGSAVVLGYTDRIGSEAYNQQL 271
              |||||||||||||||||||||||||:|:||||:|||||| ||||:||||||:|||| |
Db        121 HFTLKSDVLFNFNKATLKPEGQQALDQMYSQLSNLDPKDGSVVVLGFTDRIGSDAYNQGL 180

Qy        272 SEKRAQSVVDYLVAKGIPAGKISARGMGESNPVTGNTCDNVKARAALIDCLAPDRRVEIE 331
              ||||||||||||::|||: |||||||||||||||||||||| ||||||||||||||
Db        181 SEKRAQSVVDYLISKGIPSNKISARGMGESNPVTGNTCDNVKARPALIDCLAPDRRVEIE 240

Qy        332 VKG 334
              |||
Db        241 VKG 243


RESULT 15
I84531
outer membrane protein A - Escherichia fergusonii (ATCC 35469) (fragment)
N;Alternate names: outer membrane protein II
C;Species: Escherichia fergusonii
A;Variety: ATCC 35469
C;Date: 04-Sep-1997 #sequence_revision 07-Nov-1997 #text_change 09-Jul-2004
C;Accession: I84531
R;Lawrence, J.G.; Ochman, H.; Hartl, D.L.
J. Gen. Microbiol. 137, 1911-1921, 1991
A;Title: Molecular and evolutionary relationships among enteric bacteria.
A;Reference number: I40701; MUID:92065252; PMID:1955870
A;Accession: I84531
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-243 <RES>
A;Cross-references: UNIPROT:P24747; GB:M63351; NID:g146982; PIDN:AAA24232.1; PID:g146983
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A;Experimental source: ATCC 35469
C;Genetics:
A;Gene: ompA
C;Superfamily: outer membrane protein A
C;Keywords: membrane protein
F;103-114/Region: alanine/proline-rich

Query Match 60.8%; Score 1109; DB 2; Length 243;
Best Local Similarity 87.2%; Pred. No. 1.7e-76;
Matches 211; Conservative 13; Mismatches 18; Indels 0; Gaps 0;

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Qy          93 LTAKLGYPITDDLDIYTRLGGMVWRADSKGNYASTGVSRSEHDTGVSPVFAGGVEWAVTR 152
               |||||||||||||||||||||||||:| :   || |   |||||||||||||||:|
Db           1 LTAKLGYPITDDLDIYTRLGGMVWRADTKAHNNVTGESDKNHDTGVSPVFAGGVEWAITP 60

Qy         153 DIATRLEYQWVNNIGDAGTVGTRPDNGMLSLGVSYRFGQEDAAPVVAPAPAPAPEVATKH 212
               :|||||||| |||||| |:|||||||:|||||||||| :|||||||||||||| |||
Db          61 EIATRLEYQWTNNIGDANTIGTRPDNGLLSLGVSYRFGQGEAAPVVAPAPAPAPEVQTKH 120

Qy         213 FTLKSDVLFNFNKATLKPEGQQALDQLYTQLSNMDPKDGSAVVLGYTDRIGSEAYNQQLS 272
               |||||||||||||||||||| |||||:||||:|||||| ||||||||||:|||| ||
Db         121 FTLKSDVLFNFNKATLKPEGQAALDQLYSQLSNLDPKDGSVVVLGYTDRIGSDAYNQGLS 180

Qy         273 EKRAQSVVDYLVAKGIPAGKISARGMGESNPVTGNTCDNVKARAALIDCLAPDRRVEIEV 332
               |:||||||||::||||| |||||||||||||||||||| ||||||||||||||||
Db         181 ERRAQSVVDYLISKGIPADKISARGMGESNPVTGNTCDNVKQRAALIDCLAPDRRVEIEV 240

Qy         333 KG 334
               ||
Db         241 KG 242
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Search completed: January 19, 2005, 18:16:59
Job time : 27 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: January 19, 2005, 18:16:43 ; Search time 526 Seconds
(without alignments)
236.281 Million cell updates/sec

Title: US-09-913-772-2
Perfect score: 1823
Sequence: 1 MKAIFVLNAAPKDNTWYAGG.....DRRVEIEVKGYKEVVTQPAG 344

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1608061 seqs, 361289386 residues

Total number of hits satisfying chosen parameters: 1608061

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
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17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1823	100.0	344	14	US-10-169-953-2	Sequence 2, Appli
2	1511	82.9	346	16	US-10-467-421-90	Sequence 90, Appl
3	1511	82.9	346	16	US-10-467-421-97	Sequence 97, Appl
4	754	41.4	190	16	US-10-416-708A-24	Sequence 24, Appl
5	754	41.4	192	16	US-10-416-708A-27	Sequence 27, Appl
6	748	41.0	194	16	US-10-416-708A-10	Sequence 10, Appl
7	748	41.0	194	16	US-10-416-708A-64	Sequence 64, Appl
8	689	37.8	344	14	US-10-336-840-9	Sequence 9, Appli
9	688	37.7	344	14	US-10-336-840-6	Sequence 6, Appli
10	687	37.7	137	15	US-10-432-056-2	Sequence 2, Appli
11	687	37.7	153	9	US-09-905-176-22	Sequence 22, Appl
12	685	37.6	344	14	US-10-336-840-3	Sequence 3, Appli
13	684	37.5	344	14	US-10-336-840-1	Sequence 1, Appli
14	684	37.5	344	14	US-10-336-840-2	Sequence 2, Appli
15	684	37.5	344	14	US-10-336-840-4	Sequence 4, Appli
16	684	37.5	344	14	US-10-336-840-7	Sequence 7, Appli
17	683	37.5	344	14	US-10-336-840-10	Sequence 10, Appl
18	680.5	37.3	341	14	US-10-336-840-5	Sequence 5, Appli
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20	680.5	37.3	341	14	US-10-336-840-11	Sequence 11, Appl
21	678	37.2	344	14	US-10-336-840-12	Sequence 12, Appl
22	671	36.8	364	11	US-09-809-665A-151	Sequence 151, App
23	671	36.8	364	17	US-10-854-299-151	Sequence 151, App
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25	649.5	35.6	353	16	US-10-467-421-21	Sequence 21, Appl
26	646.5	35.5	353	14	US-10-203-942-9	Sequence 9, Appli
27	646.5	35.5	369	11	US-09-809-665A-153	Sequence 153, App
28	646.5	35.5	369	17	US-10-854-299-153	Sequence 153, App
29	643.5	35.3	352	14	US-10-336-840-37	Sequence 37, Appl
30	639.5	35.1	369	17	US-10-770-824-10	Sequence 10, Appl
31	506	27.8	356	14	US-10-336-840-38	Sequence 38, Appl
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37	251	13.8	240	16	US-10-467-421-95	Sequence 95, Appl
38	242	13.3	272	15	US-10-406-686A-13	Sequence 13, Appl
39	176.5	9.7	261	15	US-10-389-647-584	Sequence 584, App
40	176	9.7	390	14	US-10-283-024-3	Sequence 3, Appli
41	174.5	9.6	229	15	US-10-282-122A-69451	Sequence 69451, A
42	169.5	9.3	375	14	US-10-323-069A-123	Sequence 123, App
43	169	9.3	179	14	US-10-080-113-2	Sequence 2, Appli
44	168	9.2	395	14	US-10-323-069A-128	Sequence 128, App
45	167.5	9.2	375	14	US-10-323-069A-120	Sequence 120, App

ALIGNMENTS

RESULT 1
US-10-169-953-2
; Sequence 2, Application US/10169953
; Publication No. US20030044915A1
; GENERAL INFORMATION:
; APPLICANT: Thierry BAUSSANT
; APPLICANT: Pascale JEANNIN
; APPLICANT: Yves DELNESTE
; APPLICANT: FranOois LAWNY
; APPLICANT: Jean-Yves BONNEFOY
; TITLE OF INVENTION: METHOD FOR PREPARING A POLYPEPTIDE SOLUBLE IN AN AQUEOUS SOLVENT
; TITLE OF INVENTION: IN THE ABSENCE OF DETERGENT
; FILE REFERENCE: D18390
; CURRENT APPLICATION NUMBER: US/10/169,953
; CURRENT FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: FR 00 00070
; PRIOR FILING DATE: 2000-01-04
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 344
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
; FEATURE:
; OTHER INFORMATION: P40
US-10-169-953-2

Query Match 100.0%; Score 1823; DB 14; Length 344;
Best Local Similarity 100.0%; Pred. No. 3e-160;
Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         61 PYLGFEMGYDWLGRMAYKGSVDNGAFKAQGVQLTAKLGYPITDDLDIYTRLGGMVWRADS 120
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 PYLGFEMGYDWLGRMAYKGSVDNGAFKAQGVQLTAKLGYPITDDLDIYTRLGGMVWRADS 120

Qy         121 KGNYASTGVSRSEHDTGVSPVFAGGVEWAVTRDIATRLEYQWVNNIGDAGTVGTRPDNGM 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 KGNYASTGVSRSEHDTGVSPVFAGGVEWAVTRDIATRLEYQWVNNIGDAGTVGTRPDNGM 180

Qy         181 LSLGVSYRFGQEDAAPVVAPAPAPAPEVATKHFTLKSDVLFNFNKATLKPEGQQALDQLY 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 LSLGVSYRFGQEDAAPVVAPAPAPAPEVATKHFTLKSDVLFNFNKATLKPEGQQALDQLY 240

Qy         241 TQLSNMDPKDGSAVVLGYTDRIGSEAYNQQLSEKRAQSVVDYLVAKGIPAGKISARGMGE 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 TQLSNMDPKDGSAVVLGYTDRIGSEAYNQQLSEKRAQSVVDYLVAKGIPAGKISARGMGE 300

Qy         301 SNPVTGNTCDNVKARAALIDCLAPDRRVEIEVKGYKEVVTQPAG 344
                |||||||||||||||||||||||||||||||||||||||||||
Db         301 SNPVTGNTCDNVKARAALIDCLAPDRRVEIEVKGYKEVVTQPAG 344


RESULT 2
US-10-467-421-90
; Sequence 90, Application US/10467421
; Publication No. US20040116665A1
; GENERAL INFORMATION:
;  APPLICANT: Berthet, Francois-Xavier Jacques
;  APPLICANT:  Denoel, Philippe
;  APPLICANT:  Neyt, Cecile Anne
;  APPLICANT:  Poolman, Jan
;  APPLICANT:  Thonnard, Joelle
;  TITLE OF INVENTION: Vaccine Composition
;  FILE REFERENCE: B45259
;  CURRENT APPLICATION NUMBER: US/10/467,421
;  CURRENT FILING DATE:  2003-08-08
;  PRIOR APPLICATION NUMBER: PCT/EP02/01361
;  PRIOR FILING DATE: 2002-02-08
;  PRIOR APPLICATION NUMBER: GB 0103171.5
;  PRIOR FILING DATE: 2001-02-08
;  NUMBER OF SEQ ID NOS: 98
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 90
;   LENGTH: 346
;   TYPE: PRT
;   ORGANISM: E. coli
US-10-467-421-90

  Query Match             82.9%;  Score 1511;  DB 16;  Length 346;
  Best Local Similarity   84.9%;  Pred. No. 2.6e-131;
  Matches  286;  Conservative   17;  Mismatches   24;  Indels   10;  Gaps    2;

Qy           6 VLNAAPKDNTWYAGGKLGWSQYHDTGFYGNGFQNNNGPTRNDQLGAGAFGGYQVNPYLGF 65
                 |  |||||||||  | ||||||||||||       ||||||  :||||||||||||||:||
Db          18 VAQAAPKDNTWYTGAKLGWSQYHDTGFI-----NNNGPTHENQLGAGAFGGYQVNPYVGF 72

Qy          66 EMGYDWLGRMAYKGSVDNGAFKAQGVQLTAKLGYPITDDLDIYTRLGGMVWRADSKGNYA 125
                ||||||||||  |||||:|||:|||||||||||||||||||||||||||||||||:| |
Db          73 EMGYDWLGRMPYKGSVENGAYKAQGVQLTAKLGYPITDDLDIYTRLGGMVWRADTKSN-- 130

Qy         126 STGVSRSEHDTGVSPVFAGGVEWAVTRDIATRLEYQWVNNIGDAGTVGTRPDNGMLSLGV 185
                   |    |||||||||||||:|:| :|||||||||  ||||||  |:|||||||||||||
Db         131 ---VYGKNHDTGVSPVFAGGVEYAITPEIATRLEYQWTNNIGDAHTIGTRPDNGMLSLGV 187

Qy         186 SYRFGQEDAAPVVAPAPAPAPEVATKHFTLKSDVLFNFNKATLKPEGQQALDQLYTQLSN 245
                ||||||  :|||||||||||||||  |||||||||||||||||||||||||  ||||||:||||
Db         188 SYRFGQGEAAPVVAPAPAPAPEVQTKHFTLKSDVLFNFNKATLKPEGQAALDQLYSQLSN 247

Qy         246 MDPKDGSAVVLGYTDRIGSEAYNQQLSEKRAQSVVDYLVAKGIPAGKISARGMGESNPVT 305
                :||||||  ||||||||||:|||| |||:|||||||||::||||| ||||||||||||||
Db         248 LDPKDGSVVVLGYTDRIGSDAYNQGLSERRAQSVVDYLISKGIPADKISARGMGESNPVT 307

Qy         306 GNTCDNVKARAALIDCLAPDRRVEIEVKGYKEVVTQP 342
                ||||||||  |||||||||||||||||||||||| |:|||||
Db         308 GNTCDNVKQRAALIDCLAPDRRVEIEVKGIKDVVTQP 344


RESULT 3
US-10-467-421-97
; Sequence 97, Application US/10467421
; Publication No. US20040116665A1
; GENERAL INFORMATION:
;  APPLICANT: Berthet, Francois-Xavier Jacques
;  APPLICANT:  Denoel, Philippe
;  APPLICANT:  Neyt, Cecile Anne
;  APPLICANT:  Poolman, Jan
;  APPLICANT:  Thonnard, Joelle
;  TITLE OF INVENTION: Vaccine Composition
;  FILE REFERENCE: B45259
;  CURRENT APPLICATION NUMBER: US/10/467,421
;  CURRENT FILING DATE:  2003-08-08
;  PRIOR APPLICATION NUMBER: PCT/EP02/01361
;  PRIOR FILING DATE: 2002-02-08
;  PRIOR APPLICATION NUMBER: GB 0103171.5
;  PRIOR FILING DATE: 2001-02-08
;  NUMBER OF SEQ ID NOS: 98
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 97
;   LENGTH: 346
;   TYPE: PRT
;   ORGANISM: E.coli
US-10-467-421-97

  Query Match             82.9%;  Score 1511;  DB 16;  Length 346;
  Best Local Similarity   84.9%;  Pred. No. 2.6e-131;
  Matches  286;  Conservative   17;  Mismatches   24;  Indels   10;  Gaps    2;

Qy           6 VLNAAPKDNTWYAGGKLGWSQYHDTGFYGNGFQNNNGPTRNDQLGAGAFGGYQVNPYLGF 65
                 |  |||||||||  | ||||||||||||       ||||||  :||||||||||||||:||
Db          18 VAQAAPKDNTWYTGAKLGWSQYHDTGFI-----NNNGPTHENQLGAGAFGGYQVNPYVGF 72

Qy          66 EMGYDWLGRMAYKGSVDNGAFKAQGVQLTAKLGYPITDDLDIYTRLGGMVWRADSKGNYA 125
                ||||||||||  |||||:|||:|||||||||||||||||||||||||||||||||:| |
Db          73 EMGYDWLGRMPYKGSVENGAYKAQGVQLTAKLGYPITDDLDIYTRLGGMVWRADTKSN-- 130

Qy         126 STGVSRSEHDTGVSPVFAGGVEWAVTRDIATRLEYQWVNNIGDAGTVGTRPDNGMLSLGV 185
                   |    |||||||||||||:|:| :|||||||||  ||||||  |:|||||||||||||
Db         131 ---VYGKNHDTGVSPVFAGGVEYAITPEIATRLEYQWTNNIGDAHTIGTRPDNGMLSLGV 187

Qy         186 SYRFGQEDAAPVVAPAPAPAPEVATKHFTLKSDVLFNFNKATLKPEGQQALDQLYTQLSN 245
                ||||||  :|||||||||||||||  |||||||||||||||||||||||||  ||||||:||||
Db         188 SYRFGQGEAAPVVAPAPAPAPEVQTKHFTLKSDVLFNFNKATLKPEGQAALDQLYSQLSN 247

Qy         246 MDPKDGSAVVLGYTDRIGSEAYNQQLSEKRAQSVVDYLVAKGIPAGKISARGMGESNPVT 305
                :||||||  ||||||||||:|||| |||:|||||||||::||||| ||||||||||||||
Db         248 LDPKDGSVVVLGYTDRIGSDAYNQGLSERRAQSVVDYLISKGIPADKISARGMGESNPVT 307

Qy         306 GNTCDNVKARAALIDCLAPDRRVEIEVKGYKEVVTQP 342
                ||||||||  |||||||||||||||||||||||| |:|||||
Db         308 GNTCDNVKQRAALIDCLAPDRRVEIEVKGIKDVVTQP 344


RESULT 4
US-10-416-708A-24
; Sequence 24, Application US/10416708A
; Publication No. US20040161753A1
; GENERAL INFORMATION:
;  APPLICANT: Wise, John G.
;  APPLICANT:  Fromknecht, Katja
;  TITLE OF INVENTION: CREATION AND IDENTIFICATION OF PROTEINS HAVING NEW DNA BINDING
;  TITLE OF INVENTION:  SPECIFICITIES
;  FILE REFERENCE: 37779-0004
;  CURRENT APPLICATION NUMBER: US/10/416,708A
;  CURRENT FILING DATE:  2004-01-28
;  NUMBER OF SEQ ID NOS: 89
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 24
;   LENGTH: 190
```

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;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Construct
US-10-416-708A-24

  Query Match            41.4%;  Score 754;  DB 16;  Length 190;
  Best Local Similarity  79.9%;  Pred. No. 1.7e-61;
  Matches  139;  Conservative    9;  Mismatches   16;  Indels   10;  Gaps    2;

Qy          6 VLNAAPKDNTWYAGGKLGWSQYHDTGFYGNGFQNNNGPTRNDQLGAGAFGGYQVNPYLGF 65
              |  |||||||||| | ||||||||||||      ||||||  :|||||||||||||||:||
Db         20 VAQAAPKDNTWYTGAKLGWSQYHDTGFI-----NNNGPTHENQLGAGAFGGYQVNPYVGF 74

Qy         66 EMGYDWLGRMAYKGSVDNGAFKAQGVQLTAKLGYPITDDLDIYTRLGGMVWRADSKGNYA 125
              |||||||||| |||||:|||:||||||||||||||||||||||||||||||||:| |
Db         75 EMGYDWLGRMPYKGSVENGAYKAQGVQLTAKLGYPITDDLDIYTRLGGMVWRADTKSN-- 132

Qy        126 STGVSRSEHDTGVSPVFAGGVEWAVTRDIATRLEYQWVNNIGDAGTVGTRPDNG 179
                 |    |||||||||||||||:|:| :||||||||| ||||||  |:|||||||
Db        133 ---VYGKNHDTGVSPVFAGGVEYAITPEIATRLEYQWTNNIGDAHTIGTRPDNG 183


RESULT 5
US-10-416-708A-27
; Sequence 27, Application US/10416708A
; Publication No. US20040161753A1
; GENERAL INFORMATION:
;  APPLICANT: Wise, John G.
;  APPLICANT:  Fromknecht, Katja
;  TITLE OF INVENTION: CREATION AND IDENTIFICATION OF PROTEINS HAVING NEW DNA BINDING
;  TITLE OF INVENTION:  SPECIFICITIES
;  FILE REFERENCE: 37779-0004
;  CURRENT APPLICATION NUMBER: US/10/416,708A
;  CURRENT FILING DATE:  2004-01-28
;  NUMBER OF SEQ ID NOS: 89
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 27
;   LENGTH: 192
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Construct
US-10-416-708A-27

  Query Match            41.4%;  Score 754;  DB 16;  Length 192;
  Best Local Similarity  79.9%;  Pred. No. 1.7e-61;
  Matches  139;  Conservative    9;  Mismatches   16;  Indels   10;  Gaps    2;

Qy          6 VLNAAPKDNTWYAGGKLGWSQYHDTGFYGNGFQNNNGPTRNDQLGAGAFGGYQVNPYLGF 65
              |  |||||||||| | ||||||||||||      ||||||  :|||||||||||||||:||
Db         20 VAQAAPKDNTWYTGAKLGWSQYHDTGFI-----NNNGPTHENQLGAGAFGGYQVNPYVGF 74

Qy         66 EMGYDWLGRMAYKGSVDNGAFKAQGVQLTAKLGYPITDDLDIYTRLGGMVWRADSKGNYA 125
              |||||||||| |||||:|||:||||||||||||||||||||||||||||||||:| |
Db         75 EMGYDWLGRMPYKGSVENGAYKAQGVQLTAKLGYPITDDLDIYTRLGGMVWRADTKSN-- 132

Qy        126 STGVSRSEHDTGVSPVFAGGVEWAVTRDIATRLEYQWVNNIGDAGTVGTRPDNG 179
                 |    |||||||||||||||:|:| :||||||||| ||||||  |:|||||||
Db        133 ---VYGKNHDTGVSPVFAGGVEYAITPEIATRLEYQWTNNIGDAHTIGTRPDNG 183


RESULT 6
US-10-416-708A-10
; Sequence 10, Application US/10416708A
; Publication No. US20040161753A1
; GENERAL INFORMATION:
;  APPLICANT: Wise, John G.
;  APPLICANT:  Fromknecht, Katja
;  TITLE OF INVENTION: CREATION AND IDENTIFICATION OF PROTEINS HAVING NEW DNA BINDING
;  TITLE OF INVENTION:  SPECIFICITIES
;  FILE REFERENCE: 37779-0004
;  CURRENT APPLICATION NUMBER: US/10/416,708A
;  CURRENT FILING DATE:  2004-01-28
;  NUMBER OF SEQ ID NOS: 89
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
;   LENGTH: 194
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Construct
US-10-416-708A-10

  Query Match            41.0%;  Score 748;  DB 16;  Length 194;
  Best Local Similarity  79.8%;  Pred. No. 6.4e-61;
  Matches  138;  Conservative    9;  Mismatches   16;  Indels   10;  Gaps    2;

Qy          6 VLNAAPKDNTWYAGGKLGWSQYHDTGFYGNGFQNNNGPTRNDQLGAGAFGGYQVNPYLGF 65
              |  |||||||||| | ||||||||||||      ||||||  :|||||||||||||||:||
Db         20 VAQAAPKDNTWYTGAKLGWSQYHDTGFI-----NNNGPTHENQLGAGAFGGYQVNPYVGF 74

Qy         66 EMGYDWLGRMAYKGSVDNGAFKAQGVQLTAKLGYPITDDLDIYTRLGGMVWRADSKGNYA 125
              |||||||||| |||||:|||:||||||||||||||||||||||||||||||||:| |
Db         75 EMGYDWLGRMPYKGSVENGAYKAQGVQLTAKLGYPITDDLDIYTRLGGMVWRADTKSN-- 132

Qy        126 STGVSRSEHDTGVSPVFAGGVEWAVTRDIATRLEYQWVNNIGDAGTVGTRPDN 178
                 |    |||||||||||||||:|:| :||||||||| ||||||  |:||||||
Db        133 ---VYGKNHDTGVSPVFAGGVEYAITPEIATRLEYQWTNNIGDAHTIGTRPDN 182


RESULT 7
US-10-416-708A-64
; Sequence 64, Application US/10416708A
; Publication No. US20040161753A1
; GENERAL INFORMATION:
;  APPLICANT: Wise, John G.
;  APPLICANT:  Fromknecht, Katja
;  TITLE OF INVENTION: CREATION AND IDENTIFICATION OF PROTEINS HAVING NEW DNA BINDING
;  TITLE OF INVENTION:  SPECIFICITIES
;  FILE REFERENCE: 37779-0004
;  CURRENT APPLICATION NUMBER: US/10/416,708A
;  CURRENT FILING DATE:  2004-01-28
;  NUMBER OF SEQ ID NOS: 89
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 64
;   LENGTH: 194
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Construct
US-10-416-708A-64

  Query Match            41.0%;  Score 748;  DB 16;  Length 194;
  Best Local Similarity  79.8%;  Pred. No. 6.4e-61;
  Matches  138;  Conservative    9;  Mismatches   16;  Indels   10;  Gaps    2;

Qy          6 VLNAAPKDNTWYAGGKLGWSQYHDTGFYGNGFQNNNGPTRNDQLGAGAFGGYQVNPYLGF 65
              |  |||||||||| | ||||||||||||      ||||||  :|||||||||||||||:||
Db         20 VAQAAPKDNTWYTGAKLGWSQYHDTGFI-----NNNGPTHENQLGAGAFGGYQVNPYVGF 74

Qy         66 EMGYDWLGRMAYKGSVDNGAFKAQGVQLTAKLGYPITDDLDIYTRLGGMVWRADSKGNYA 125
              |||||||||| |||||:|||:||||||||||||||||||||||||||||||||:| |
Db         75 EMGYDWLGRMPYKGSVENGAYKAQGVQLTAKLGYPITDDLDIYTRLGGMVWRADTKSN-- 132

Qy        126 STGVSRSEHDTGVSPVFAGGVEWAVTRDIATRLEYQWVNNIGDAGTVGTRPDN 178
                 |    |||||||||||||||:|:| :||||||||| ||||||  |:||||||
Db        133 ---VYGKNHDTGVSPVFAGGVEYAITPEIATRLEYQWTNNIGDAHTIGTRPDN 182


RESULT 8
US-10-336-840-9
; Sequence 9, Application US/10336840
; Publication No. US20030219454A1
; GENERAL INFORMATION:
;  APPLICANT: TERRY, TAMSIN DEBORAH
```

```
;  APPLICANT:  TSENG, HSING-JU
;  APPLICANT:  HOBB, RHONDA IVY
;  APPLICANT:  JENNINGS, MICHAEL PAUL
;  APPLICANT:  DOWNES, JOHN
;  TITLE OF INVENTION: HAEMAGGLUTININ ANTIGEN
;  FILE REFERENCE: 37955-0007
;  CURRENT APPLICATION NUMBER: US/10/336,840
;  CURRENT FILING DATE:  2003-01-06
;  PRIOR APPLICATION NUMBER: PCT/AU01/00822
;  PRIOR FILING DATE: 2001-07-06
;  NUMBER OF SEQ ID NOS: 39
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
;   LENGTH: 344
;   TYPE: PRT
;   ORGANISM: Haemophilus paragallinarum
US-10-336-840-9

  Query Match            37.8%;  Score 689;  DB 14;  Length 344;
  Best Local Similarity  44.9%;  Pred. No. 4.2e-55;
  Matches  153;  Conservative   46;  Mismatches  124;  Indels   18;  Gaps    7;

Qy          1 MKAIFVLNAAPKDNTWYAGGKLGWSQYHDTGFYGNGFQNNNGPTRNDQLGAGAFGGYQVN 60
              : |  |  |||: ||:||| | ||: :||        || :|  ||  :  | |||||:
Db         13 LTAASVAQAAPQANTFYAGAKAGWASFHDGLNQFENSQNADGTLRN-SVTYGVFGGYQIT 71

Qy         61 PYLGFEMGYDWLGRMAYK-GSVDNGAFKAQGVQLTAKLGYPITDDLDIYTRLGGMVWRAD 119
                   |:|||  ||   : |      :   |  |: |  ||: : ||:| |:|  : |:|
Db         72 DNFAVELGYDDFGRAKLRQGGETVIKYTNHGAHLSLKASYPVLEGLDVYARVGAALIRSD 131

Qy        120 SKGNYASTGVSRSEHDTGVSPVFAGGVEWAVTR--DIATRLEYQWVNNIG----DAGTVG 173
               |    :      ||   |||||||:|: :    ::| |:|||||| :|    |   |
Db        132 YKPTKRAAPNQTHEHSLKVSPVFAGGLEYNLPSLPELALRVEYQWVNKVGRVEKDGSRVD 191

Qy        174 TRPDNGMLSLGVSYRFGQEDAAPVVAPAPAPAPEVATKHFTLKSDVLFNFNKATLKPEGQ 233
               |  | :: |:||||||  :|||       |:|  | | | ||| | | || |:|| |
Db        192 YTPSIGSVTAGLSYRFGQ--SAPVV------EPKVVAKTFALNSDVTFAFGKANLRPEAQ 243

Qy        234 QALDQLYTQLSNMDPKDGSAVVLGYTDRIGSEAYNQQLSEKRAQSVVDYLVAKGIPAGKI 293
               || :| ::: :  |      | |||||||||| | :||::|| :| :|||:||:    |
Db        244 NVLDGIYGEIAQL--KSVQVDVAGYTDRIGSEAANLKLSQRRADTVANYLVSKGVAQEVI 301

Qy        294 SARGMGESNPVTGNTCDNVKARAALIDCLAPDRRVEIEVKG 334
               |: | ||:|||||  || || | ||| ||| |||||| |||
Db        302 SSTGYGEANPVTGAKCDTVKGRKALIACLADDRRVEISVKG 342


RESULT 9
US-10-336-840-6
; Sequence 6, Application US/10336840
; Publication No. US20030219454A1
; GENERAL INFORMATION:
;  APPLICANT: TERRY, TAMSIN DEBORAH
;  APPLICANT:  TSENG, HSING-JU
;  APPLICANT:  HOBB, RHONDA IVY
;  APPLICANT:  JENNINGS, MICHAEL PAUL
;  APPLICANT:  DOWNES, JOHN
;  TITLE OF INVENTION: HAEMAGGLUTININ ANTIGEN
;  FILE REFERENCE: 37955-0007
;  CURRENT APPLICATION NUMBER: US/10/336,840
;  CURRENT FILING DATE:  2003-01-06
;  PRIOR APPLICATION NUMBER: PCT/AU01/00822
;  PRIOR FILING DATE: 2001-07-06
;  NUMBER OF SEQ ID NOS: 39
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
;   LENGTH: 344
;   TYPE: PRT
;   ORGANISM: Haemophilus paragallinarum
US-10-336-840-6

  Query Match            37.7%;  Score 688;  DB 14;  Length 344;
  Best Local Similarity  44.9%;  Pred. No. 5.3e-55;
  Matches  153;  Conservative   46;  Mismatches  124;  Indels   18;  Gaps    7;

Qy          1 MKAIFVLNAAPKDNTWYAGGKLGWSQYHDTGFYGNGFQNNNGPTRNDQLGAGAFGGYQVN 60
              : |  |  |||: ||:||| | ||: :||        || :|  ||  :  | |||||:
Db         13 LTAASVAQAAPQANTFYAGAKAGWASFHDGLNQFENSQNADGTLRN-SVTYGVFGGYQIT 71

Qy         61 PYLGFEMGYDWLGRMAYK-GSVDNGAFKAQGVQLTAKLGYPITDDLDIYTRLGGMVWRAD 119
                   |:|||  ||   : |      :   |  |: |  ||: : ||:| |:|  : |:|
Db         72 DNFAVELGYDDFGRAKRRQGGETVIKYTNHGAHLSLKASYPVLEGLDVYARVGAALIRSD 131

Qy        120 SKGNYASTGVSRSEHDTGVSPVFAGGVEWAVTR--DIATRLEYQWVNNIG----DAGTVG 173
               |    :      ||   |||||||:|: :    ::| |:|||||| :|    |   |
Db        132 YKPTKRAAPNQTHEHSLKVSPVFAGGLEYNLPSLPELALRVEYQWVNKVGRVEKDGSRVD 191

Qy        174 TRPDNGMLSLGVSYRFGQEDAAPVVAPAPAPAPEVATKHFTLKSDVLFNFNKATLKPEGQ 233
               |  | :: |:||||||  :|||       |:|  | | | ||| | | || |:|| |
Db        192 YTPSIGSVTAGLSYRFGQ--SAPVV------EPKVVAKTFALNSDVTFAFGKANLRPEAQ 243

Qy        234 QALDQLYTQLSNMDPKDGSAVVLGYTDRIGSEAYNQQLSEKRAQSVVDYLVAKGIPAGKI 293
               || :| ::: :  |      | |||||||||| | :||::|| :| :|||:||:    |
Db        244 NVLDGIYGEIAQL--KSVQVDVAGYTDRIGSEAANLKLSQRRADTVANYLVSKGVAQEVI 301

Qy        294 SARGMGESNPVTGNTCDNVKARAALIDCLAPDRRVEIEVKG 334
               |: | ||:|||||  || || | ||| ||| |||||| |||
Db        302 SSTGYGEANPVTGAKCDTVKGRKALIACLADDRRVEISVKG 342


RESULT 10
US-10-432-056-2
; Sequence 2, Application US/10432056
; Publication No. US20040014661A1
; GENERAL INFORMATION:
;  APPLICANT: GOETSCH, Liliane
;  APPLICANT: HAEUW, Jean-Francois
;  APPLICANT: ROBERT, Alain
;  TITLE OF INVENTION: PERIPLASMIC DOMAIN OF AN ENTEROBACTERIUM OMP PROTEIN
;  TITLE OF INVENTION:  AND ITS USE AS CARRIER OR ADJUVANT
;  FILE REFERENCE: 344 667 - US
;  CURRENT APPLICATION NUMBER: US/10/432,056
;  CURRENT FILING DATE:  2003-05-16
;  PRIOR APPLICATION NUMBER: PCT/FR 01/03 596
;  PRIOR FILING DATE: 2001-11-16
;  PRIOR APPLICATION NUMBER: FR 00/14 909
;  PRIOR FILING DATE: 2000-11-17
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 137
;   TYPE: PRT
;   ORGANISM: Klebsiella pneumoniae
US-10-432-056-2

  Query Match            37.7%;  Score 687;  DB 15;  Length 137;
  Best Local Similarity  100.0%;  Pred. No. 1.8e-55;
  Matches  135;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        208 VATKHFTLKSDVLFNFNKATLKPEGQQALDQLYTQLSNMDPKDGSAVVLGYTDRIGSEAY 267
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 VATKHFTLKSDVLFNFNKATLKPEGQQALDQLYTQLSNMDPKDGSAVVLGYTDRIGSEAY 60

Qy        268 NQQLSEKRAQSVVDYLVAKGIPAGKISARGMGESNPVTGNTCDNVKARAALIDCLAPDRR 327
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 NQQLSEKRAQSVVDYLVAKGIPAGKISARGMGESNPVTGNTCDNVKARAALIDCLAPDRR 120

Qy        328 VEIEVKGYKEVVTQP 342
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Db        121 VEIEVKGYKEVVTQP 135


RESULT 11
US-09-905-176-22
; Sequence 22, Application US/09905176
; Patent No. US20020150906A1
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; GENERAL INFORMATION:
;  APPLICANT: CALIFORNIA INSTITUTE OF TECHNOLOGY
;  APPLICANT:  Debe, Derek A.
;  TITLE OF INVENTION: METHOD FOR DETERMINING THREE-DIMENSIONAL PROTEIN STRUCTURE FROM P
;  TITLE OF INVENTION:  PROTEIN SEQUENCE
;  FILE REFERENCE: 265/297
;  CURRENT APPLICATION NUMBER: US/09/905,176
;  CURRENT FILING DATE:  2002-04-05
;  PRIOR APPLICATION NUMBER: US 60/218,016
;  PRIOR FILING DATE: 2000-07-12
;  NUMBER OF SEQ ID NOS: 26
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 22
;   LENGTH: 153
;   TYPE: PRT
;   ORGANISM: Escherichia coli
US-09-905-176-22

  Query Match            37.7%;  Score 687;  DB 9;  Length 153;
  Best Local Similarity  79.1%;  Pred. No. 2.1e-55;
  Matches  129;  Conservative   10;  Mismatches   14;  Indels   10;  Gaps    2;

Qy         27 YHDTGFYGNGFQNNNGPTRNDQLGAGAFGGYQVNPYLGFEMGYDWLGRMAYKGSVDNGAF 86
              |||||       ||||||  ::|||||||||||||:|||||||||||| |||||:|||:
Db          1 YHDTGLI-----NNNGPTHENKLGAGAFGGYQVNPYVGFEMGYDWLGRMPYKGSVENGAY 55

Qy         87 KAQGVQLTAKLGYPITDDLDIYTRLGGMVWRADSKGNYASTGVSRSEHDTGVSPVFAGGV 146
              ||||||||||||||||||||||||||||||:  |     |    ||||||||||||
Db         56 KAQGVQLTAKLGYPITDDLDIYTRLGGMVWRADTYSN-----VYGKNHDTGVSPVFAGGV 110

Qy        147 EWAVTRDIATRLEYQWVNNIGDAGTVGTRPDNGMLSLGVSYRF 189
              |:|:| :|||||||| |||||| |:||||||||||||||||
Db        111 EYAITPEIATRLEYQWTNNIGDAHTIGTRPDNGMLSLGVSYRF 153


RESULT 12
US-10-336-840-3
; Sequence 3, Application US/10336840
; Publication No. US20030219454A1
; GENERAL INFORMATION:
;  APPLICANT: TERRY, TAMSIN DEBORAH
;  APPLICANT:  TSENG, HSING-JU
;  APPLICANT:  HOBB, RHONDA IVY
;  APPLICANT:  JENNINGS, MICHAEL PAUL
;  APPLICANT:  DOWNES, JOHN
;  TITLE OF INVENTION: HAEMAGGLUTININ ANTIGEN
;  FILE REFERENCE: 37955-0007
;  CURRENT APPLICATION NUMBER: US/10/336,840
;  CURRENT FILING DATE:  2003-01-06
;  PRIOR APPLICATION NUMBER: PCT/AU01/00822
;  PRIOR FILING DATE: 2001-07-06
;  NUMBER OF SEQ ID NOS: 39
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 344
;   TYPE: PRT
;   ORGANISM: Haemophilus paragallinarum
US-10-336-840-3

  Query Match            37.6%;  Score 685;  DB 14;  Length 344;
  Best Local Similarity  44.9%;  Pred. No. 1e-54;
  Matches  153;  Conservative   46;  Mismatches  124;  Indels   18;  Gaps    7;

Qy          1 MKAIFVLNAAPKDNTWYAGGKLGWSQYHDTGFYGNGFQNNNGPTRNDQLGAGAFGGYQVN 60
              : |  | :|||: ||:||| | ||: :||        || :|  ||  :  | |||||:
Db         13 LTAASVAQAAPQANTFYAGAKAGWASFHDGLNQFENSQNADGTLRN-SVTYGVFGGYQIT 71

Qy         61 PYLGFEMGYDWLGR-MAYKGSVDNGAFKAQGVQLTAKLGYPITDDLDIYTRLGGMVWRAD 119
                  |:|||  ||  : :|          |  |: |  ||: : ||:|  |:|  : |:|
Db         72 DNFAVELGYDDFGRAKSRQGGETVIKHTNHGAHLSLKASYPVLEGLDVYARVGAALIRSD 131

Qy        120 SKGNYASTGVSRSEHDTGVSPVFAGGVEWAVTR--DIATRLEYQWVNNIG----DAGTVG 173
               |    :      ||   ||||||||:|: :    ::| |:|||||| :|    |   |
Db        132 YKPTKRAAPNQTHEHSLKVSPVFAGGLEYNLPSLPELALRVEYQWVNKVGRVEKDGSRVD 191

Qy        174 TRPDNGMLSLGVSYRFGQEDAAPVVAPAPAPAPEVATKHFTLKSDVLFNFNKATLKPEGQ 233
               |  | :: |:||||||  :||||        |:|  | | | ||| | | || |:|| |
Db        192 YTPSIGSVTAGLSYRFGQ--SAPVV------EPKVVAKTFALNSDVTFAFGKANLRPEAQ 243

Qy        234 QALDQLYTQLSNMDPKDGSAVVLGYTDRIGSEAYNQQLSEKRAQSVVDYLVAKGIPAGKI 293
               || :| ::: :  |      | |||||||||| | :||::|| :| :|||:||:    |
Db        244 NVLDGIYGEIAQL--KSVQVDVAGYTDRIGSEAANLKLSQRRADTVANYLVSKGVAQEVI 301

Qy        294 SARGMGESNPVTGNTCDNVKARAALIDCLAPDRRVEIEVKG 334
               |: | ||:|||||  || || | ||| ||| |||||| |||
Db        302 SSTGYGEANPVTGAKCDTVKGRKALIACLADDRRVEISVKG 342


RESULT 13
US-10-336-840-1
; Sequence 1, Application US/10336840
; Publication No. US20030219454A1
; GENERAL INFORMATION:
;  APPLICANT: TERRY, TAMSIN DEBORAH
;  APPLICANT:  TSENG, HSING-JU
;  APPLICANT:  HOBB, RHONDA IVY
;  APPLICANT:  JENNINGS, MICHAEL PAUL
;  APPLICANT:  DOWNES, JOHN
;  TITLE OF INVENTION: HAEMAGGLUTININ ANTIGEN
;  FILE REFERENCE: 37955-0007
;  CURRENT APPLICATION NUMBER: US/10/336,840
;  CURRENT FILING DATE:  2003-01-06
;  PRIOR APPLICATION NUMBER: PCT/AU01/00822
;  PRIOR FILING DATE: 2001-07-06
;  NUMBER OF SEQ ID NOS: 39
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 344
;   TYPE: PRT
;   ORGANISM: Haemophilus paragallinarum
US-10-336-840-1

  Query Match            37.5%;  Score 684;  DB 14;  Length 344;
  Best Local Similarity  44.6%;  Pred. No. 1.2e-54;
  Matches  152;  Conservative   46;  Mismatches  125;  Indels   18;  Gaps    7;

Qy          1 MKAIFVLNAAPKDNTWYAGGKLGWSQYHDTGFYGNGFQNNNGPTRNDQLGAGAFGGYQVN 60
              : |  | :|||: ||:||| | ||: :||        ||  |  ||  :  | |||||:
Db         13 LTAASVAQAAPQANTFYAGAKAGWASFHDGLNQFENSQNAYGTLRN-SVTYGVFGGYQIT 71

Qy         61 PYLGFEMGYDWLGRMAYKGSVDN-GAFKAQGVQLTAKLGYPITDDLDIYTRLGGMVWRAD 119
                  |:|||  ||   :   :  |      |  |: |  ||: : ||:|  |:|  : |:|
Db         72 DNFAVELGYDDFGRAKLRQDGETVGKHTNHGAHLSLKASYPVLEGLDVYARVGAALIRSD 131

Qy        120 SKGNYASTGVSRSEHDTGVSPVFAGGVEWAVTR--DIATRLEYQWVNNIG----DAGTVG 173
               |    :      ||   ||||||||:|: :    ::| |:|||||| :|    |   |
Db        132 YKPTKRAAPNETHEHSLKVSPVFAGGLEYNLPSLPELALRVEYQWVNKVGRWEKDGSRVD 191

Qy        174 TRPDNGMLSLGVSYRFGQEDAAPVVAPAPAPAPEVATKHFTLKSDVLFNFNKATLKPEGQ 233
               |  | :: |:||||||  :||||        |:|  | | | ||| | | || |:|| |
Db        192 YTPSIGSVTAGLSYRFGQ--SAPVV------EPKVVAKTFALNSDVTFAFGKANLRPEAQ 243

Qy        234 QALDQLYTQLSNMDPKDGSAVVLGYTDRIGSEAYNQQLSEKRAQSVVDYLVAKGIPAGKI 293
               || :| ::: :  |      : ||||||||| | :||::|| :| :|||:||:    |
Db        244 NVLDGIYGEIAQL--KSVQVDLAGYTDRIGSEAANLKLSQRRADTVANYLVSKGVAQEVI 301

Qy        294 SARGMGESNPVTGNTCDNVKARAALIDCLAPDRRVEIEVKG 334
               |: | ||:|||||  || || | ||| ||| |||||| |||
Db        302 SSTGYGEANPVTGAKCDAVKGRKALIACLADDRRVEISVKG 342


RESULT 14
US-10-336-840-2
; Sequence 2, Application US/10336840
; Publication No. US20030219454A1
; GENERAL INFORMATION:
```

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;  APPLICANT: TERRY, TAMSIN DEBORAH
;  APPLICANT:  TSENG, HSING-JU
;  APPLICANT:  HOBB, RHONDA IVY
;  APPLICANT:  JENNINGS, MICHAEL PAUL
;  APPLICANT:  DOWNES, JOHN
;  TITLE OF INVENTION: HAEMAGGLUTININ ANTIGEN
;  FILE REFERENCE: 37955-0007
;  CURRENT APPLICATION NUMBER: US/10/336,840
;  CURRENT FILING DATE:  2003-01-06
;  PRIOR APPLICATION NUMBER: PCT/AU01/00822
;  PRIOR FILING DATE: 2001-07-06
;  NUMBER OF SEQ ID NOS: 39
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 344
;   TYPE: PRT
;   ORGANISM: Haemophilus paragallinarum
US-10-336-840-2

  Query Match            37.5%;  Score 684;  DB 14;  Length 344;
  Best Local Similarity   44.6%;  Pred. No. 1.2e-54;
  Matches  152;  Conservative   46;  Mismatches  125;  Indels   18;  Gaps    7;

Qy          1 MKAIFVLNAAPKDNTWYAGGKLGWSQYHDTGFYGNGFQNNNGPTRNDQLGAGAFGGYQVN 60
              : |  |  |||: ||:||| | ||: :||         ||  |  ||  :  | |||||:
Db         13 LTAASVAQAAPQANTFYAGAKAGWASFHDGLNQFENSQNAYGTLRN-SVTYGVFGGYQIT 71

Qy         61 PYLGFEMGYDWLGRMAYKGSVDN-GAFKAQGVQLTAKLGYPITDDLDIYTRLGGMVWRAD 119
                 |:|||  ||   :   :  |     |  |: |  ||: : ||:| |:|  : |:|
Db         72 DNFAVELGYDDFGRAKLRQDGETVGKHTNHGAHLSLKASYPVLEGLDVYARVGAALIRSD 131

Qy        120 SKGNYASTGVSRSEHDTGVSPVFAGGVEWAVTR--DIATRLEYQWVNNIG----DAGTVG 173
               |    :      ||   ||||||||:|: :    ::| |:|||||| :|    |   |
Db        132 YKPTKRAAPNETHEHSLKVSPVFAGGLEYNLPSLPELALRVEYQWVNKVGRWEKDGSRVD 191

Qy        174 TRPDNGMLSLGVSYRFGQEDAAPVVAPAPAPAPEVATKHFTLKSDVLFNFNKATLKPEGQ 233
                 |  | :: |:||||||  :||||       |:|  | | | ||| | | || |:|| |
Db        192 YTPSIGSVTAGLSYRFGQ--SAPVV------EPKVVAKTFALNSDVTFAFGKANLRPEAQ 243

Qy        234 QALDQLYTQLSNMDPKDGSAVVLGYTDRIGSEAYNQQLSEKRAQSVVDYLVAKGIPAGKI 293
                || :| ::: :  |     : ||||||||| | :||::|| :| :|||:||:    |
Db        244 NVLDGIYGEIAQL--KSVQVDLAGYTDRIGSEAANLKLSQRRADTVANYLVSKGVAQEVI 301

Qy        294 SARGMGESNPVTGNTCDNVKARAALIDCLAPDRRVEIEVKG 334
              |: | ||:|||||  || || | ||| ||| |||||| |||
Db        302 SSTGYGEANPVTGAKCDAVKGRKALIACLADDRRVEISVKG 342


RESULT 15
US-10-336-840-4
; Sequence 4, Application US/10336840
; Publication No. US20030219454A1
; GENERAL INFORMATION:
;  APPLICANT: TERRY, TAMSIN DEBORAH
;  APPLICANT:  TSENG, HSING-JU
;  APPLICANT:  HOBB, RHONDA IVY
;  APPLICANT:  JENNINGS, MICHAEL PAUL
;  APPLICANT:  DOWNES, JOHN
;  TITLE OF INVENTION: HAEMAGGLUTININ ANTIGEN
;  FILE REFERENCE: 37955-0007
;  CURRENT APPLICATION NUMBER: US/10/336,840
;  CURRENT FILING DATE:  2003-01-06
;  PRIOR APPLICATION NUMBER: PCT/AU01/00822
;  PRIOR FILING DATE: 2001-07-06
;  NUMBER OF SEQ ID NOS: 39
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
;   LENGTH: 344
;   TYPE: PRT
;   ORGANISM: Haemophilus paragallinarum
US-10-336-840-4

  Query Match            37.5%;  Score 684;  DB 14;  Length 344;
  Best Local Similarity   44.6%;  Pred. No. 1.2e-54;
  Matches  152;  Conservative   46;  Mismatches  125;  Indels   18;  Gaps    7;

Qy          1 MKAIFVLNAAPKDNTWYAGGKLGWSQYHDTGFYGNGFQNNNGPTRNDQLGAGAFGGYQVN 60
              : |  |  |||: ||:||| | ||: :||         ||  |  ||  :  | |||||:
Db         13 LTAASVAQAAPQANTFYAGAKAGWASFHDGLNQFENSQNAYGTLRN-SVTYGVFGGYQIT 71

Qy         61 PYLGFEMGYDWLGRMAYKGSVDN-GAFKAQGVQLTAKLGYPITDDLDIYTRLGGMVWRAD 119
                 |:|||  ||   :   :  |     |  |: |  ||: : ||:| |:|  : |:|
Db         72 DNFAVELGYDDFGRAKLRQDGETVGKHTNHGAHLSLKASYPVLEGLDVYARVGAALIRSD 131

Qy        120 SKGNYASTGVSRSEHDTGVSPVFAGGVEWAVTR--DIATRLEYQWVNNIG----DAGTVG 173
               |    :      ||   ||||||||:|: :    ::| |:|||||| :|    |   |
Db        132 YKPTKRAAPNETHEHSLKVSPVFAGGLEYNLPSLPELALRVEYQWVNKVGRWEKDGSRVD 191

Qy        174 TRPDNGMLSLGVSYRFGQEDAAPVVAPAPAPAPEVATKHFTLKSDVLFNFNKATLKPEGQ 233
                 |  | :: |:||||||  :||||       |:|  | | | ||| | | || |:|| |
Db        192 YTPSIGSVTAGLSYRFGQ--SAPVV------EPKVVAKTFALNSDVTFAFGKANLRPEAQ 243

Qy        234 QALDQLYTQLSNMDPKDGSAVVLGYTDRIGSEAYNQQLSEKRAQSVVDYLVAKGIPAGKI 293
                || :| ::: :  |     : ||||||||| | :||::|| :| :|||:||:    |
Db        244 NVLDGIYGEIAQL--KSVQVDLAGYTDRIGSEAANLKLSQRRADTVANYLVSKGVAQEVI 301

Qy        294 SARGMGESNPVTGNTCDNVKARAALIDCLAPDRRVEIEVKG 334
              |: | ||:|||||  || || | ||| ||| |||||| |||
Db        302 SSTGYGEANPVTGAKCDAVKGRKALIACLADDRRVEISVKG 342


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Job time : 531 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: January 19, 2005, 18:02:20 ; Search time 24 Seconds
(without alignments)
950.558 Million cell updates/sec

Title: US-09-913-772-2
Perfect score: 1823
Sequence: 1 MKAIFVLNAAPKDNTWYAGG.....DRRVEIEVKGYKEVVTQPAG 344

Scoring table: BLOSUM62
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Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1782	97.8	385	4	US-09-489-039A-7451	Sequence 7451, Ap
2	1781	97.7	335	3	US-08-836-500A-2	Sequence 2, Appli
3	1781	97.7	335	4	US-09-679-750-2	Sequence 2, Appli
4	1279	70.2	384	4	US-09-543-681A-7922	Sequence 7922, Ap
5	984	54.0	179	3	US-08-836-500A-4	Sequence 4, Appli
6	984	54.0	179	4	US-09-679-750-4	Sequence 4, Appli
7	671	36.8	364	4	US-09-809-665A-151	Sequence 151, App
8	667	36.6	364	4	US-09-418-980-8	Sequence 8, Appli
9	662.5	36.3	359	1	US-08-457-997B-2	Sequence 2, Appli
10	662.5	36.3	359	3	US-08-467-722A-2	Sequence 2, Appli
11	662.5	36.3	359	4	US-09-451-184-2	Sequence 2, Appli
12	646.5	35.5	369	4	US-09-809-665A-153	Sequence 153, App
13	639.5	35.1	369	4	US-09-418-980-10	Sequence 10, Appl
14	586.5	32.2	338	1	US-08-210-394-1	Sequence 1, Appli
15	379	20.8	72	3	US-08-836-500A-6	Sequence 6, Appli
16	379	20.8	72	4	US-09-679-750-6	Sequence 6, Appli
17	281	15.4	53	3	US-08-836-500A-8	Sequence 8, Appli
18	281	15.4	53	4	US-09-679-750-8	Sequence 8, Appli
19	242.5	13.3	379	4	US-09-328-352-5219	Sequence 5219, Ap
20	231.5	12.7	351	4	US-09-252-991A-30094	Sequence 30094, A
21	224.5	12.3	349	4	US-09-573-630A-2	Sequence 2, Appli
22	199	10.9	235	4	US-09-252-991A-19595	Sequence 19595, A
23	193.5	10.6	259	4	US-09-328-352-5775	Sequence 5775, Ap
24	184.5	10.1	566	4	US-09-489-039A-14179	Sequence 14179, A
25	182	10.0	220	4	US-09-489-039A-11012	Sequence 11012, A
26	182	10.0	226	2	US-08-572-447C-15	Sequence 15, Appl
27	182	10.0	226	3	US-09-267-747-15	Sequence 15, Appl
28	181	9.9	161	2	US-08-572-447C-11	Sequence 11, Appl
29	181	9.9	161	3	US-09-267-747-11	Sequence 11, Appl
30	176.5	9.7	266	4	US-09-252-991A-18046	Sequence 18046, A
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32	175	9.6	753	4	US-09-252-991A-17612	Sequence 17612, A
33	170	9.3	472	4	US-09-328-352-6870	Sequence 6870, Ap
34	169.5	9.3	272	4	US-09-252-991A-29681	Sequence 29681, A
35	168.5	9.2	214	2	US-08-572-447C-13	Sequence 13, Appl
36	168.5	9.2	214	3	US-09-267-747-13	Sequence 13, Appl
37	165.5	9.1	417	4	US-09-252-991A-26245	Sequence 26245, A
38	163.5	9.0	169	4	US-09-252-991A-19373	Sequence 19373, A
39	161	8.8	278	4	US-09-328-352-5824	Sequence 5824, Ap
40	158	8.7	257	4	US-09-328-352-6621	Sequence 6621, Ap
41	149	8.2	231	4	US-09-540-236-3827	Sequence 3827, Ap
42	146.5	8.0	172	4	US-09-674-779B-6	Sequence 6, Appli
43	143.5	7.9	172	4	US-09-674-779B-8	Sequence 8, Appli
44	142.5	7.8	152	4	US-09-540-236-3190	Sequence 3190, Ap
45	142.5	7.8	172	4	US-09-674-779B-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-09-489-039A-7451
; Sequence 7451, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 7451
; LENGTH: 385
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-7451

Query Match 97.8%; Score 1782; DB 4; Length 385;
Best Local Similarity 99.4%; Pred. No. 5e-169;
Matches 336; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy          6 VLNAAPKDNTWYAGGKLGWSQYHDTGFYGNGFQNNNGPTRNDQLGAGAFGGYQVNPYLGF 65
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Qy         66 EMGYDWLGRMAYKGSVDNGAFKAQGVQLTAKLGYPITDDLDIYTRLGGMVWRADSKGNYA 125
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        107 EMGYDWLGRMAYKGSVDNGAFKAQGVQLTAKLGYPITDDLDIYTRLGGMVWRADSKGNYA 166

Qy        126 STGVSRSEHDTGVSPVFAGGVEWAVTRDIATRLEYQWVNNIGDAGTVGTRPDNGMLSLGV 185
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        167 STGVSRSEHDTGVSPVFAGGVEWAVTRDIATRLEYQWVNNIGDAGTVGTRPDNGMLSLGV 226

Qy        186 SYRFGQEDAAPVVAPAPAPAPEVATKHFTLKSDVLFNFNKATLKPEGQQALDQLYTQLSN 245
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        227 SYRFGQEDAAPVVAPAPAPAPEVATKHFTLKSDVLFNFNKATLKPEGQQALDQLYTQLSN 286

Qy        246 MDPKDGSAVVLGYTDRIGSEAYNQQLSEKRAQSVVDYLVAKGIPAGKISARGMGESNPVT 305
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        287 MDPKDGSAVVLGYTDRIGSEAYNQQLSEKRAQSVVDYLVAKGIPAGKISARGMGESNPVT 346

Qy        306 GNTCDNVKARAALIDCLAPDRRVEIEVKGYKEVVTQPA 343
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Db        347 GNTCDNVKARAALIDCLAPDRRVEIEVKGYKEVVTQPA 384
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RESULT 2

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US-08-836-500A-2
; Sequence 2, Application US/08836500A
; Patent No. 6197929
;  GENERAL INFORMATION:
;    APPLICANT:  Binz, Hans
;    APPLICANT:  Baussant, Thierry
;    APPLICANT:  Haeuw, Jean-Francois
;    APPLICANT:  Nguyen Ngoc, Thien
;    TITLE OF INVENTION:  Carrier Protein Having an Adjuvant
;    TITLE OF INVENTION:  Effect, Immunogenic Complex Containing It, Process for
;    TITLE OF INVENTION:  Their Preparation, Nucleotide Sequence and Vaccines
; Patent No. 6197929
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Rockey, Milnamow & Katz, Ltd.
;      STREET:  180 N. Stetson, 2 Prudential Plaza, Suite
;      STREET:  4700
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  U.S.A.
;      ZIP:  60601
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/836,500A
;      FILING DATE:
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Katz, Martin L.
;      REGISTRATION NUMBER:  25,011
;      REFERENCE/DOCKET NUMBER:  PIE1514P0180US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312-616-5400
;      TELEFAX:  312-616-5460
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  335 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-836-500A-2

  Query Match             97.7%;  Score 1781;  DB 3;  Length 335;
  Best Local Similarity   100.0%;  Pred. No. 5.1e-169;
  Matches  335;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          10 APKDNTWYAGGKLGWSQYHDTGFYGNGFQNNNGPTRNDQLGAGAFGGYQVNPYLGFEMGY 69
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 APKDNTWYAGGKLGWSQYHDTGFYGNGFQNNNGPTRNDQLGAGAFGGYQVNPYLGFEMGY 60

Qy          70 DWLGRMAYKGSVDNGAFKAQGVQLTAKLGYPITDDLDIYTRLGGMVWRADSKGNYASTGV 129
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 DWLGRMAYKGSVDNGAFKAQGVQLTAKLGYPITDDLDIYTRLGGMVWRADSKGNYASTGV 120

Qy         130 SRSEHDTGVSPVFAGGVEWAVTRDIATRLEYQWVNNIGDAGTVGTRPDNGMLSLGVSYRF 189
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 SRSEHDTGVSPVFAGGVEWAVTRDIATRLEYQWVNNIGDAGTVGTRPDNGMLSLGVSYRF 180

Qy         190 GQEDAAPVVAPAPAPAPEVATKHFTLKSDVLFNFNKATLKPEGQQALDQLYTQLSNMDPK 249
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 GQEDAAPVVAPAPAPAPEVATKHFTLKSDVLFNFNKATLKPEGQQALDQLYTQLSNMDPK 240

Qy         250 DGSAVVLGYTDRIGSEAYNQQLSEKRAQSVVDYLVAKGIPAGKISARGMGESNPVTGNTC 309
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 DGSAVVLGYTDRIGSEAYNQQLSEKRAQSVVDYLVAKGIPAGKISARGMGESNPVTGNTC 300

Qy         310 DNVKARAALIDCLAPDRRVEIEVKGYKEVVTQPAG 344
               ||||||||||||||||||||||||||||||||||
Db         301 DNVKARAALIDCLAPDRRVEIEVKGYKEVVTQPAG 335
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RESULT 3
US-09-679-750-2
; Sequence 2, Application US/09679750
; Patent No. 6780420
;   GENERAL INFORMATION:
;        APPLICANT: Binz, Hans
;                   Baussant, Thierry
;                   Haeuw, Jean-Francois
;                   Nguyen Ngoc, Thien
;        TITLE OF INVENTION: Carrier Protein Having an Adjuvant
;                            Effect, Immunogenic Complex Containing It, Process for
;                            Their Preparation, Nucleotide Sequence and Vaccines
; Patent No. 6780420
;        NUMBER OF SEQUENCES: 8
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Rockey, Milnamow & Katz, Ltd.
;             STREET: 180 N. Stetson, 2 Prudential Plaza, Suite
;                     4700
;             CITY: Chicago
;             STATE: Illinois
;             COUNTRY: U.S.A.
;             ZIP: 60601
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/679,750
;             FILING DATE: 08-Oct-2000
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/836,500
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Katz, Martin L.
;             REGISTRATION NUMBER: 25,011
;             REFERENCE/DOCKET NUMBER: PIE1514P0180US
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 312-616-5400
;             TELEFAX: 312-616-5460
;   INFORMATION FOR SEQ ID NO: 2:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 335 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-679-750-2

  Query Match             97.7%;  Score 1781;  DB 4;  Length 335;
  Best Local Similarity   100.0%;  Pred. No. 5.1e-169;
  Matches  335;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          10 APKDNTWYAGGKLGWSQYHDTGFYGNGFQNNNGPTRNDQLGAGAFGGYQVNPYLGFEMGY 69
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 APKDNTWYAGGKLGWSQYHDTGFYGNGFQNNNGPTRNDQLGAGAFGGYQVNPYLGFEMGY 60

Qy          70 DWLGRMAYKGSVDNGAFKAQGVQLTAKLGYPITDDLDIYTRLGGMVWRADSKGNYASTGV 129
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 DWLGRMAYKGSVDNGAFKAQGVQLTAKLGYPITDDLDIYTRLGGMVWRADSKGNYASTGV 120

Qy         130 SRSEHDTGVSPVFAGGVEWAVTRDIATRLEYQWVNNIGDAGTVGTRPDNGMLSLGVSYRF 189
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 SRSEHDTGVSPVFAGGVEWAVTRDIATRLEYQWVNNIGDAGTVGTRPDNGMLSLGVSYRF 180

Qy         190 GQEDAAPVVAPAPAPAPEVATKHFTLKSDVLFNFNKATLKPEGQQALDQLYTQLSNMDPK 249
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 GQEDAAPVVAPAPAPAPEVATKHFTLKSDVLFNFNKATLKPEGQQALDQLYTQLSNMDPK 240

Qy         250 DGSAVVLGYTDRIGSEAYNQQLSEKRAQSVVDYLVAKGIPAGKISARGMGESNPVTGNTC 309
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        241 DGSAVVLGYTDRIGSEAYNQQLSEKRAQSVVDYLVAKGIPAGKISARGMGESNPVTGNTC 300

Qy        310 DNVKARAALIDCLAPDRRVEIEVKGYKEVVTQPAG 344
              ||||||||||||||||||||||||||||||||||
Db        301 DNVKARAALIDCLAPDRRVEIEVKGYKEVVTQPAG 335


RESULT 4
US-09-543-681A-7922
; Sequence 7922, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
;  APPLICANT: GARY BRETON
;  TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL
;  TITLE OF INVENTION:  DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE: 2709.1002-001
;  CURRENT APPLICATION NUMBER: US/09/543,681A
;  CURRENT FILING DATE:  2000-04-05
;  PRIOR APPLICATION NUMBER: US 60/128,706
;  PRIOR FILING DATE: 1999-04-09
;  NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 7922
;   LENGTH: 384
;   TYPE: PRT
;   ORGANISM: Proteus mirabilis
US-09-543-681A-7922

  Query Match            70.2%;  Score 1279;  DB 4;  Length 384;
  Best Local Similarity  71.5%;  Pred. No. 6.7e-119;
  Matches  243;  Conservative   32;  Mismatches   59;  Indels    6;  Gaps    3;

Qy          9 AAPKDNTWYAGGKLGWSQYHDTGFYGNGFQNNNGPTRNDQLGAGAFGGYQVNPYLGFEMG 68
              |||||||||  |||||||||   ||    :|     || |   ||:||||| ||| | |||||:|
Db         43 AAPKDNTWYTGGKLGWSQYQSTGNNWDGVNIGNGSTHKDQIGAGAFAGYQYNQYLGFELG 102

Qy         69 YDWLGRMAYKGSVDNGAFKAQGVQLTAKLGYPITDDLDIYTRLGGMVWRADSKG--NYAS 126
              |||||||||||| :||||||||:||| || ||: ||||:|||||||||||||     |  |
Db        103 YDWLGRMAYKGSYNNGAFKAQGIQLTTKLSYPVMDDLDVYTRLGGMVWRADSTATINATS 162

Qy        127 TGVSR--SEHDTGVSPVFAGGVEWAVTRDIATRLEYQWVNNIGDAGTVGTRPDNGMLSLG 184
                |  :  ||:|||||||| | |:|:| :|||||||:||||| ||:  ||||||||:|
Db        163 AGTQKRFSENDTGVSPVFALGTEYAITPNIATRLEYQWINNIGDKGTLNARPDNGMLSVG 222

Qy        185 VSYRFGQEDAAPVVAPAP--APAPEVATKHFTLKSDVLFNFNKATLKPEGQQALDQLYTQ 242
              |:||| ||  |||| |||  |||| |   | |||:||||||:||::|| |||:||: || :
Db        223 VAYRFNQETPAPVVEPAPVVAPAPVVENKTFTLRSDVLFNYNKSSLKAEGQEALNGLYNE 282

Qy        243 LSNMDPKDGSAVVLGYTDRIGSEAYNQQLSEKRAQSVVDYLVAKGIPAGKISARGMGESN 302
              |:|:||  |  ||:|||||||: ||  |||||||||||||:|||||  ||| | |: |
Db        283 LANIDPTQGRVVVIGYTDRIGSQNYNLPLSEKRAQSVVDYLVSKGIPANSISAEGRGKEN 342

Qy        303 PVTGNTCDNVKARAALIDCLAPDRRVEIEVKGYKEVVTQP 342
              |||||||||:|||||||||||||||||::|  ||| ||
Db        343 PVTGNTCDNIKARAALIDCLAPDRRVEIEIQGTTEVVVQP 382


RESULT 5
US-08-836-500A-4
; Sequence 4, Application US/08836500A
; Patent No. 6197929
;  GENERAL INFORMATION:
;    APPLICANT:  Binz, Hans
;    APPLICANT:  Baussant, Thierry
;    APPLICANT:  Haeuw, Jean-Francois
;    APPLICANT:  Nguyen Ngoc, Thien
;    TITLE OF INVENTION:  Carrier Protein Having an Adjuvant
;    TITLE OF INVENTION:  Effect, Immunogenic Complex Containing It, Process for
;    TITLE OF INVENTION:  Their Preparation, Nucleotide Sequence and Vaccines
; Patent No. 6197929
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Rockey, Milnamow & Katz, Ltd.
;      STREET:  180 N. Stetson, 2 Prudential Plaza, Suite
;      STREET:  4700
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  U.S.A.
;      ZIP:  60601
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/836,500A
;      FILING DATE:
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Katz, Martin L.
;      REGISTRATION NUMBER:  25,011
;      REFERENCE/DOCKET NUMBER:  PIE1514P0180US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312-616-5400
;      TELEFAX:  312-616-5460
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  179 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-836-500A-4

  Query Match            54.0%;  Score 984;  DB 3;  Length 179;
  Best Local Similarity  100.0%;  Pred. No. 5.3e-90;
  Matches  179;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         10 APKDNTWYAGGKLGWSQYHDTGFYGNGFQNNNGPTRNDQLGAGAFGGYQVNPYLGFEMGY 69
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 APKDNTWYAGGKLGWSQYHDTGFYGNGFQNNNGPTRNDQLGAGAFGGYQVNPYLGFEMGY 60

Qy         70 DWLGRMAYKGSVDNGAFKAQGVQLTAKLGYPITDDLDIYTRLGGMVWRADSKGNYASTGV 129
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DWLGRMAYKGSVDNGAFKAQGVQLTAKLGYPITDDLDIYTRLGGMVWRADSKGNYASTGV 120

Qy        130 SRSEHDTGVSPVFAGGVEWAVTRDIATRLEYQWVNNIGDAGTVGTRPDNGMLSLGVSYR 188
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SRSEHDTGVSPVFAGGVEWAVTRDIATRLEYQWVNNIGDAGTVGTRPDNGMLSLGVSYR 179


RESULT 6
US-09-679-750-4
; Sequence 4, Application US/09679750
; Patent No. 6780420
;   GENERAL INFORMATION:
;        APPLICANT: Binz, Hans
;                   Baussant, Thierry
;                   Haeuw, Jean-Francois
;                   Nguyen Ngoc, Thien
;        TITLE OF INVENTION: Carrier Protein Having an Adjuvant
;                            Effect, Immunogenic Complex Containing It, Process for
;                            Their Preparation, Nucleotide Sequence and Vaccines
; Patent No. 6780420
;        NUMBER OF SEQUENCES: 8
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Rockey, Milnamow & Katz, Ltd.
;             STREET: 180 N. Stetson, 2 Prudential Plaza, Suite
;                  4700
;             CITY: Chicago
;             STATE: Illinois
;             COUNTRY: U.S.A.
;             ZIP: 60601
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
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;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/679,750
;             FILING DATE: 08-Oct-2000
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/836,500
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Katz, Martin L.
;             REGISTRATION NUMBER: 25,011
;             REFERENCE/DOCKET NUMBER: PIE1514P0180US
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 312-616-5400
;             TELEFAX: 312-616-5460
;    INFORMATION FOR SEQ ID NO: 4:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 179 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-679-750-4

  Query Match             54.0%;  Score 984;  DB 4;  Length 179;
  Best Local Similarity   100.0%;  Pred. No. 5.3e-90;
  Matches  179;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         10 APKDNTWYAGGKLGWSQYHDTGFYGNGFQNNNGPTRNDQLGAGAFGGYQVNPYLGFEMGY 69
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 APKDNTWYAGGKLGWSQYHDTGFYGNGFQNNNGPTRNDQLGAGAFGGYQVNPYLGFEMGY 60

Qy         70 DWLGRMAYKGSVDNGAFKAQGVQLTAKLGYPITDDLDIYTRLGGMVWRADSKGNYASTGV 129
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DWLGRMAYKGSVDNGAFKAQGVQLTAKLGYPITDDLDIYTRLGGMVWRADSKGNYASTGV 120

Qy        130 SRSEHDTGVSPVFAGGVEWAVTRDIATRLEYQWVNNIGDAGTVGTRPDNGMLSLGVSYR 188
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SRSEHDTGVSPVFAGGVEWAVTRDIATRLEYQWVNNIGDAGTVGTRPDNGMLSLGVSYR 179


RESULT 7
US-09-809-665A-151
; Sequence 151, Application US/09809665A
; Patent No. 6790950
; GENERAL INFORMATION:
;  APPLICANT: Lowery E., David, et al.
;  TITLE OF INVENTION: Anti-Bacterial Vaccine Compositions
;  FILE REFERENCE: 28341/00435
;  CURRENT APPLICATION NUMBER: US/09/809,665A
;  CURRENT FILING DATE:  2001-03-15
;  PRIOR APPLICATION NUMBER: 60/153,453
;  PRIOR FILING DATE: 1999-09-10
;  PRIOR APPLICATION NUMBER: 60/128,689
;  PRIOR FILING DATE: 1999-04-09
;  PRIOR APPLICATION NUMBER: 09/545,199
;  PRIOR FILING DATE: 2000-04-06
;  NUMBER OF SEQ ID NOS: 197
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 151
;   LENGTH: 364
;   TYPE: PRT
;   ORGANISM: Actinobacillus pleuropneumoniae
US-09-809-665A-151

  Query Match             36.8%;  Score 671;  DB 4;  Length 364;
  Best Local Similarity   42.4%;  Pred. No. 2.4e-58;
  Matches  153;  Conservative   54;  Mismatches  122;  Indels   32;  Gaps   10;

Qy          1 MKAIFVLNAAPKDNTWYAGGKLGWSQYHDTGFYGNGFQNNNGPTR----NDQLGAGAFGG 56
              : |  |  |||: ||:||| | ||: :||     :  :| :  |:     : :  | |||
Db         11 LSAAAVAQAAPQQNTFYAGAKAGWASFHDGIEQLDSAKNTDRGTKYGINRNSVTYGVFGG 70

Qy         57 YQV--NPYLGF--EMGYDWLGRM----AYKGSVDNGAFK--AQGVQLTAKLGYPITDDLD 106
              ||:     ||   |:|||: ||:       |  |   |:  | |  :  |  | :  |||
Db         71 YQILNQDKLGLAAELGYDYFGRVRGSEKPNGKADKKTFRHAAHGATIALKPSYEVLPDLD 130

Qy        107 IYTRLG-GMVWRADSKGNYASTGVSRSEHDTGVSPVFAGGVEWAVTRDIATRLEYQWVNN 165
              :| ::|  :|     | |  |     :  | :   |||:|:  ::| |:||||:||
Db        131 VYGKVGIALVNNTYKTFNAAQEKVKTRRFQS--SLILGAGVEYAILPELAARVEYQWLNN 188

Qy        166 IGDA--------GTVGTRPDNGMLSLGVSYRFGQEDAAPVVAPAPAPAPEVATKHFTLKS 217
              | |         |   | |  :| |:|||||  |||| |||      | ||:|   |
Db        189 AGKASYSTLNRMGATDYRSDISSVSAGLSYRFGQ-GAAPVAAPA------VETKNFAFSS 241

Qy        218 DVLFNFNKATLKPEGQQALDQLYTQLSNMDPKDGSAVVLGYTDRIGSEAYNQQLSEKRAQ 277
              |||| | |: |||    ||| : |:::|    : :  | ||||||| || | :||::||:
Db        242 DVLFAFGKSNLKPAAATALDAMQTEINNAGLSNAAIQVNGYTDRIGKEASNLKLSQRRAE 301

Qy        278 SVVDYLVAKGIPAGKISARGMGESNPVTGNTCDNVKARAALIDCLAPDRRVEIEVKGYKE 337
              :| :|:|:|| ||  ::| | ||:||||| ||| || | ||| |||||||||::|:| ||
Db        302 TVANYIVSKGAPAANVTAVGYGEANPVTGATCDKVKGRKALIACLAPDRRVEVQVQGTKE 361

Qy        338 V 338
              |
Db        362 V 362


RESULT 8
US-09-418-980-8
; Sequence 8, Application US/09418980
; Patent No. 6713071
; GENERAL INFORMATION:
;  APPLICANT: Campos, Manuel
;  APPLICANT: Baarsch, Mary Jo
;  APPLICANT: Rosey, Everett
;  APPLICANT: Ankenbauer, Robert
;  APPLICANT: Warren-Stewart, Lynn
;  APPLICANT: Suiter, Brian
;  APPLICANT: Keach, Robin
;  TITLE OF INVENTION: NOVEL PROTEINS FROM ACTINOBACILLUS PLEUROPNEUMONIAE
;  FILE REFERENCE: PC9854A
;  CURRENT APPLICATION NUMBER: US/09/418,980
;  CURRENT FILING DATE: 1999-10-14
;  NUMBER OF SEQ ID NOS: 96
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
;   LENGTH: 364
;   TYPE: PRT
;   ORGANISM: Actinobacillus pleuropneumoniae
US-09-418-980-8

  Query Match             36.6%;  Score 667;  DB 4;  Length 364;
  Best Local Similarity   42.1%;  Pred. No. 6.1e-58;
  Matches  152;  Conservative   54;  Mismatches  123;  Indels   32;  Gaps   10;

Qy          1 MKAIFVLNAAPKDNTWYAGGKLGWSQYHDTGFYGNGFQNNNGPTR----NDQLGAGAFGG 56
              : |  |  |||: ||:||| | ||: :||     :  :| :  |:     : :  | |||
Db         11 LSAAAVAQAAPQQNTFYAGAKAGWASFHDGIEQLDSAKNTDRGTKYGINRNSVTYGVFGG 70

Qy         57 YQV--NPYLGF--EMGYDWLGRM----AYKGSVDNGAFK--AQGVQLTAKLGYPITDDLD 106
              ||:     ||   |:|||: ||:       |  |   |:  | |  :  |  | :  |||
Db         71 YQILNQDKLGLAAELGYDYFGRVRGSEKPNGKADKKTFRHAAHGATIALKPSYEVLPDLD 130

Qy        107 IYTRLG-GMVWRADSKGNYASTGVSRSEHDTGVSPVFAGGVEWAVTRDIATRLEYQWVNN 165
              :| ::|  :|     | |  |     :  | :   |||:|:  ::| |:||||:||
Db        131 VYGKVGIALVNNTYKTFNAAQEKVKTRRFQS--SLILGAGVEYAILPELAARVEYQWLNN 188

Qy        166 IGDA--------GTVGTRPDNGMLSLGVSYRFGQEDAAPVVAPAPAPAPEVATKHFTLKS 217
              | |         |   | |  :| |:|||||  |||| |||      | ||:|   |
Db        189 AGKASYSTLNRMGATDYRSDISSVSAGLSYRFGQ-GAVPVAAPA------VETKNFAFSS 241

Qy        218 DVLFNFNKATLKPEGQQALDQLYTQLSNMDPKDGSAVVLGYTDRIGSEAYNQQLSEKRAQ 277
              |||| | |: |||    ||| : |:::|    : :  | ||||||| || | :||::||:
Db        242 DVLFAFGKSNLKPAAATALDAMQTEINNAGLSNAAIQVNGYTDRIGKEASNLKLSQRRAE 301

Qy        278 SVVDYLVAKGIPAGKISARGMGESNPVTGNTCDNVKARAALIDCLAPDRRVEIEVKGYKE 337
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Db        302 TVANYIVSKGAPAANVTAVGYGEANPVTGATCDKVKGRKALIACLAPDRRVEVQVQGTKE 361

Qy        338 V 338
              |
Db        362 V 362


RESULT 9
US-08-457-997B-2
; Sequence 2, Application US/08457997B
; Patent No. 5766608
;  GENERAL INFORMATION:
;    APPLICANT:  Kolattukudy, P. E.
;    TITLE OF INVENTION:  Otitis Media Vaccine
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Calfee, Halter and Griswold
;      STREET:  Suite 1800 800 Superior Avenue
;      CITY:  Cleveland
;      STATE:  Ohio
;      COUNTRY:  U.S.A.
;      ZIP:  44114-2688
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/457,997B
;      FILING DATE:
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Golrick, Mary E.
;      REGISTRATION NUMBER:  34,829
;      REFERENCE/DOCKET NUMBER:  22727/00102
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (216) 622-8458
;      TELEFAX:  (216) 241-0816
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  359 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-457-997B-2

  Query Match             36.3%;  Score 662.5;  DB 1;  Length 359;
  Best Local Similarity   43.3%;  Pred. No. 1.7e-57;
  Matches  155;  Conservative   49;  Mismatches  121;  Indels   33;  Gaps    9;

Qy          1 MKAIFVLNAAPKDNTWYAGGKLGWSQYHD----TGFYGNGFQNNNGPTRNDQLGAGAFGG 56
              : |  | |||::||:||| | |   :||     |    |  ::|   | :    | |||
Db         13 LAAASVAQAAPQENTFYAGVKAGQGSFHDGINNNGAIKKGLSSSNYGYRRNTFTYGVFGG 72

Qy         57 YQV----NPYLGFEMGYDWLGRMAYKGSVDNGAFKAQ----GVQLTAKLGYPITDDLDIY 108
              ||:    |  |  |:||| ||   :  : |  ||:    |  |: |  | : | ||:|
Db         73 YQILNQDNFGLAAELGYDDFGRAKLR---EAGKPKAKHTNHGAYLSLKGSYEVLDGLDVY 129

Qy        109 TRLGGMVWRADSKGNYASTGV---SRSEHDTGVSPVFAGGVEWAVTRDIATRLEYQWVNN 165
              : |  : |:| |    : |     :  |    | :|| | |:||  ::| ||||||:
Db        130 GKAGVALVRSDYKFYEDANGTRDHKKGRHTARASGLFAVGAEYAVLPELAVRLEYQWLTR 189

Qy        166 IG-------DAGTVGTRPDNGMLSLGVSYRFGQEDAAPVVAPAPAPAPEVATKHFTLKSD 218
              :|            :   |  | :: |:|||||| : |||||     |||: :| |:| ||
Db        190 VGKYRPQDKPNTAINYNPWIGCINAGISYRFGQGE-APVVA-----APEMVSKTFSLNSD 243

Qy        219 VLFNFNKATLKPEGQQALDQLYTQLSNMDPKDGSAVVLGYTDRIGSEAYNQQLSEKRAQS 278
              | | | || |||: |  || :| ::| :  |      | |||:||||:|:| :||::|| |
Db        244 VTFAFGKANLKPQAQATLDSVYGEISQV--KSRKVAVAGYTNRIGSDAFNVKLSQERADS 301

Qy        279 VVDYLVAKGIPAGKISARGMGESNPVTGNTCDNVKARAALIDCLAPDRRVEIEVKGYK 336
              | :| ||||: |  ||| | ||:||||| ||| || | ||| ||||||||| | | |
Db        302 VANYFVAKGVAADAISATGYGEANPVTGATCDQVKGRKALIACLAPDRRVEIAVNGTK 359


RESULT 10
US-08-467-722A-2
; Sequence 2, Application US/08467722A
; Patent No. 6030626
;  GENERAL INFORMATION:
;    APPLICANT:  Kolattukudy, P. E.
;    TITLE OF INVENTION:  Otitis Media Vaccine
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Calfee, Halter and Griswold
;      STREET:  Suite 1800 800 Superior Avenue
;      CITY:  Cleveland
;      STATE:  Ohio
;      COUNTRY:  U.S.A>
;      ZIP:  44114-2688
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/467,722A
;      FILING DATE:
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Golrick, Mary E.
;      REGISTRATION NUMBER:  34,829
;      REFERENCE/DOCKET NUMBER:  22727/00102
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (216) 622-8458
;      TELEFAX:  (216) 241-0816
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  359 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-467-722A-2

  Query Match             36.3%;  Score 662.5;  DB 3;  Length 359;
  Best Local Similarity   43.3%;  Pred. No. 1.7e-57;
  Matches  155;  Conservative   49;  Mismatches  121;  Indels   33;  Gaps    9;

Qy          1 MKAIFVLNAAPKDNTWYAGGKLGWSQYHD----TGFYGNGFQNNNGPTRNDQLGAGAFGG 56
              : |  | |||::||:||| | |   :||     |    |  ::|   | :    | |||
Db         13 LAAASVAQAAPQENTFYAGVKAGQGSFHDGINNNGAIKKGLSSSNYGYRRNTFTYGVFGG 72

Qy         57 YQV----NPYLGFEMGYDWLGRMAYKGSVDNGAFKAQ----GVQLTAKLGYPITDDLDIY 108
              ||:    |  |  |:||| ||   :  : |  ||:    |  |: |  | : | ||:|
Db         73 YQILNQDNFGLAAELGYDDFGRAKLR---EAGKPKAKHTNHGAYLSLKGSYEVLDGLDVY 129

Qy        109 TRLGGMVWRADSKGNYASTGV---SRSEHDTGVSPVFAGGVEWAVTRDIATRLEYQWVNN 165
              : |  : |:| |    : |     :  |    | :|| | |:||  ::| ||||||:
Db        130 GKAGVALVRSDYKFYEDANGTRDHKKGRHTARASGLFAVGAEYAVLPELAVRLEYQWLTR 189

Qy        166 IG-------DAGTVGTRPDNGMLSLGVSYRFGQEDAAPVVAPAPAPAPEVATKHFTLKSD 218
              :|            :   |  | :: |:|||||| : |||||     |||: :| |:| ||
Db        190 VGKYRPQDKPNTAINYNPWIGCINAGISYRFGQGE-APVVA-----APEMVSKTFSLNSD 243

Qy        219 VLFNFNKATLKPEGQQALDQLYTQLSNMDPKDGSAVVLGYTDRIGSEAYNQQLSEKRAQS 278
              | | | || |||: |  || :| ::| :  |      | |||:||||:|:| :||::|| |
Db        244 VTFAFGKANLKPQAQATLDSVYGEISQV--KSRKVAVAGYTNRIGSDAFNVKLSQERADS 301

Qy        279 VVDYLVAKGIPAGKISARGMGESNPVTGNTCDNVKARAALIDCLAPDRRVEIEVKGYK 336
              | :| ||||: |  ||| | ||:||||| ||| || | ||| ||||||||| | | |
Db        302 VANYFVAKGVAADAISATGYGEANPVTGATCDQVKGRKALIACLAPDRRVEIAVNGTK 359


RESULT 11
US-09-451-184-2
```

```
; Sequence 2, Application US/09451184
; Patent No. 6562349
;  GENERAL INFORMATION:
;    APPLICANT:  Kolattukudy, P. E.
;    TITLE OF INVENTION:  Otitis Media Vaccine
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Calfee, Halter and Griswold
;      STREET:  1400 McDonald Investment Center,
;      STREET:  800 Superior Avenue
;      CITY:  Cleveland
;      STATE:  Ohio
;      COUNTRY:  U.S.A>
;      ZIP:  44114-2688
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/451,184
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Docherty, Pamela A.
;      REGISTRATION NUMBER:  40,591
;      REFERENCE/DOCKET NUMBER:  24547/04000
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (216) 622-8416
;      TELEFAX:  (216) 241-0816
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  359 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-451-184-2

  Query Match             36.3%;  Score 662.5;  DB 4;  Length 359;
  Best Local Similarity   43.3%;  Pred. No. 1.7e-57;
  Matches  155;  Conservative   49;  Mismatches  121;  Indels   33;  Gaps    9;

Qy          1 MKAIFVLNAAPKDNTWYAGGKLGWSQYHD----TGFYGNGFQNNNGPTRNDQLGAGAFGG 56
              : |  |  |||::||:||| | |   :||     |    |  ::|   | :    | |||
Db         13 LAAASVAQAAPQENTFYAGVKAGQGSFHDGINNNGAIKKGLSSSNYGYRRNTFTYGVFGG 72

Qy         57 YQV----NPYLGFEMGYDWLGRMAYKGSVDNGAFKAQ----GVQLTAKLGYPITDDLDIY 108
              ||:    |  |  |:||| ||   :  : |  ||:     |  |: |  | : | ||:|
Db         73 YQILNQDNFGLAAELGYDDFGRAKLR---EAGKPKAKHTNHGAYLSLKGSYEVLDGLDVY 129

Qy        109 TRLGGMVWRADSKGNYASTGV---SRSEHDTGVSPVFAGGVEWAVTRDIATRLEYQWVNN 165
               : |  : |:| |    : |     :  |    | :|| | |:||  ::| ||||||:
Db        130 GKAGVALVRSDYKFYEDANGTRDHKKGRHTARASGLFAVGAEYAVLPELAVRLEYQWLTR 189

Qy        166 IG-------DAGTVGTRPDNGMLSLGVSYRFGQEDAAPVVAPAPAPAPEVATKHFTLKSD 218
              :|           :   |  | :: |:|||||| : |||||     |||: :| |:| ||
Db        190 VGKYRPQDKPNTAINYNPWIGCINAGISYRFGQGE-APVVA-----APEMVSKTFSLNSD 243

Qy        219 VLFNFNKATLKPEGQQALDQLYTQLSNMDPKDGSAVVLGYTDRIGSEAYNQQLSEKRAQS 278
              | | | || |||: |  || :| ::| :  |     | |||:||||:|:| :||::|| |
Db        244 VTFAFGKANLKPQAQATLDSVYGEISQV--KSRKVAVAGYTNRIGSDAFNVKLSQERADS 301

Qy        279 VVDYLVAKGIPAGKISARGMGESNPVTGNTCDNVKARAALIDCLAPDRRVEIEVKGYK 336
              | :| ||||: |  ||| | ||:||||| ||| || | ||| ||||||||||| | | |
Db        302 VANYFVAKGVAADAISATGYGEANPVTGATCDQVKGRKALIACLAPDRRVEIAVNGTK 359


RESULT 12
US-09-809-665A-153
; Sequence 153, Application US/09809665A
; Patent No. 6790950
; GENERAL INFORMATION:
;  APPLICANT: Lowery E., David, et al.
;  TITLE OF INVENTION: Anti-Bacterial Vaccine Compositions
;  FILE REFERENCE: 28341/00435
;  CURRENT APPLICATION NUMBER: US/09/809,665A
;  CURRENT FILING DATE:  2001-03-15
;  PRIOR APPLICATION NUMBER: 60/153,453
;  PRIOR FILING DATE: 1999-09-10
;  PRIOR APPLICATION NUMBER: 60/128,689
;  PRIOR FILING DATE: 1999-04-09
;  PRIOR APPLICATION NUMBER: 09/545,199
;  PRIOR FILING DATE: 2000-04-06
;  NUMBER OF SEQ ID NOS: 197
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 153
;   LENGTH: 369
;   TYPE: PRT
;   ORGANISM: Actinobacillus pleuropneumoniae
US-09-809-665A-153

  Query Match             35.5%;  Score 646.5;  DB 4;  Length 369;
  Best Local Similarity   41.1%;  Pred. No. 6.9e-56;
  Matches  153;  Conservative   60;  Mismatches  110;  Indels   49;  Gaps   12;

Qy          1 MKAIFVLNAAPKDNTWYAGGKLGWSQYHDTGFYG-NGFQNNNGPTRNDQ----------L 49
              : |  |  |||: ||:||| |:| | :|    :| |  :: :    ||:          :
Db         11 LSAAAVAQAAPQQNTFYAGAKVGQSSFH----HGVNQLKSGHDDRYNDKTRKYGINRNSV 66

Qy         50 GAGAFGGYQV----NPYLGFEMGYDWLGRMAYKGSVDNGAFK-----AQGVQLTAKLGYP 100
                | |||||:    |  |  |:|||: ||:  :|:||   |:     | |: |  |  |
Db         67 TYGVFGGYQILNQNNFGLAAELGYDYYGRV--RGNVDE--FRTVKHSAHGLNLALKPSYE 122

Qy        101 ITDDLDIYTRLGGMVWRADSKGNYASTGVSRSE---HDTGVSPVFAGGVEWAVTRDIATR 157
              :  |||:| ::|  | | | |  | :  : |     |    | :  |||:|:  ::| |
Db        123 VLPDLDVYGKVGIAVVRNDYK-KYGAENTNESTTKFHKLKASTILGAGVEYAILPELAAR 181

Qy        158 LEYQWVNNIGDAGTV----GTR-------PDNGMLSLGVSYRFGQEDAAPVVAPAPAPAP 206
              :|||::|  |:        ||:       ||   :: |:||||||   ||||       |
Db        182 VEYQYLNKAGNLNKALVRSGTQDVDFQYAPDIHSVTAGLSYRFGQGAVAPVV------EP 235

Qy        207 EVATKHFTLKSDVLFNFNKATLKPEGQQALDQLYTQLSNMDPKDGSAVVLGYTDRIGSEA 266
              || ||:|   |||||:| |::|||    |||   |:::|:     :  | ||||||| ||
Db        236 EVVTKNFAFSSDVLFDFGKSSLKPAAATALDAANTEIANLGLATPAIQVNGYTDRIGKEA 295

Qy        267 YNQQLSEKRAQSVVDYLVAKGIPAGKISARGMGESNPVTGNTCDNVKARAALIDCLAPDR 326
              | :|||::||::| :|||:||     ::| | ||:|||| ||| || | ||| ||||||
Db        296 SNLKLSQRRAETVANYLVSKGQNPANVTAVGYGEANPVTGATCDAVKGRKALIACLAPDR 355

Qy        327 RVEIEVKGYKEV 338
              |||::|:| | |
Db        356 RVEVQVQGAKNV 367


RESULT 13
US-09-418-980-10
; Sequence 10, Application US/09418980
; Patent No. 6713071
; GENERAL INFORMATION:
;  APPLICANT: Campos, Manuel
;  APPLICANT: Baarsch, Mary Jo
;  APPLICANT: Rosey, Everett
;  APPLICANT: Ankenbauer, Robert
;  APPLICANT: Warren-Stewart, Lynn
;  APPLICANT: Suiter, Brian
;  APPLICANT: Keach, Robin
;  TITLE OF INVENTION: NOVEL PROTEINS FROM ACTINOBACILLUS PLEUROPNEUMONIAE
;  FILE REFERENCE: PC9854A
;  CURRENT APPLICATION NUMBER: US/09/418,980
;  CURRENT FILING DATE: 1999-10-14
;  NUMBER OF SEQ ID NOS: 96
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
;   LENGTH: 369
;   TYPE: PRT
;   ORGANISM: Actinobacillus pleuropneumoniae
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US-09-418-980-10

Query Match 35.1%; Score 639.5; DB 4; Length 369;
Best Local Similarity 40.7%; Pred. No. 3.4e-55;
Matches 151; Conservative 60; Mismatches 113; Indels 47; Gaps 11;

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Qy          1 MKAIFVLNAAPKDNTWYAGGKLGWSQYHDTGFYG-NGFQNNNGPTRNDQ----------L 49
              : |  |  |||: ||:||| |:| | :|    :| |  :: :    ||:           :
Db         11 LSAAAVAQAAPQQNTFYAGAKVGQSSFH----HGVNQLKSGHDDRYNDKTRKYGINRNSV 66

Qy         50 GAGAFGGYQV----NPYLGFEMGYDWLGRMAYKGSVDNGAFK-----AQGVQLTAKLGYP 100
                | |||||:    |  |  |:|||: ||:  :|  ::| |:     | |:    |  |
Db         67 TYGVFGGYQILNQNNFGLATELGYDYYGRV--RG--NDGEFRAMKHSAHGLNFALKPSYE 122

Qy        101 ITDDLDIYTRLGGMVWRADSKGNYASTGVSRSE--HDTGVSPVFAGGVEWAVTRDIATRL 158
              :  ||:| ::|  | | | |    |       :|  |    | :   |||:|:  ::| |:
Db        123 VLPDLDVYGKVGVAVVRNDYKSYGAENTNEPTEKFHKLKASTILGAGVEYAILPELAARV 182

Qy        159 EYQWVNNIGDAGTV----GTR-------PDNGMLSLGVSYRFGQEDAAPVVAPAPAPAPE 207
              |||::|  |:        ||:       ||   :: |:|||||   ||||       ||
Db        183 EYQYLNKAGNLNKALVRSGTQDVDFQYAPDIHSVTAGLSYRFGQGAVAPVV------EPE 236

Qy        208 VATKHFTLKSDVLFNFNKATLKPEGQQALDQLYTQLSNMDPKDGSAVVLGYTDRIGSEAY 267
              | ||:|   |||||:| |::|||    |||   |:::|:     :  | |||||||  ||
Db        237 VVTKNFAFSSDVLFDFGKSSLKPAAATALDAANTEIANLGLATPAIQVNGYTDRIGKEAS 296

Qy        268 NQQLSEKRAQSVVDYLVAKGIPAGKISARGMGESNPVTGNTCDNVKARAALIDCLAPDRR 327
              | :||::||::| :|||:||     ::| | ||:|||| ||| || | ||| |||||||
Db        297 NLKLSQRRAETVANYLVSKGQNPANVTAVGYGEANPVTGATCDKVKGRKALIACLAPDRR 356

Qy        328 VEIEVKGYKEV 338
              ||::|:| | |
Db        357 VEVQVQGAKNV 367
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RESULT 14
US-08-210-394-1
; Sequence 1, Application US/08210394
; Patent No. 5770213
; GENERAL INFORMATION:
; APPLICANT: Zlotnick Dr., Gary W.
; TITLE OF INVENTION: Purified No. 5770213typable Haemophilus
; TITLE OF INVENTION: influenzae P5 Protein as a Vaccine for No. 5770213typable
; TITLE OF INVENTION: Haemophilus Influenzae Strain
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Cyanamid Company
; STREET: One Cyanamid Plaza
; CITY: Wayne
; STATE: New Jersey
; COUNTRY: US
; ZIP: 07470-8426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/210,394
; FILING DATE: 07-MAR-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Harrington, James J
; REFERENCE/DOCKET NUMBER: 32,144
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201/831-3246
; TELEFAX: 201/831-3305
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 338 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-210-394-1

Query Match 32.2%; Score 586.5; DB 1; Length 338;
Best Local Similarity 40.1%; Pred. No. 5.8e-50;
Matches 146; Conservative 44; Mismatches 111; Indels 63; Gaps 12;

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Qy         10 APKDNTWYAGGKLGWSQYHDTGFYGNGFQNNNGPTRNDQLGA-------------GAFGG 56
              ||::||:||| | |   :||      |  ||||  : | :                 | |||
Db          1 APQENTFYAGVKAGQGSFHD------GI-NNNGAIKEDSIDLTLGYGYRRNTFTYGVFGG 53

Qy         57 YQV----NPYLGFEMGYDWLGRMAYKGSVDNGAFKAQ----GVQLTAKLGYPITDDLDIY 108
              ||:    |  |  |:|||  ||: ::     |  ||:    |  |: |  | : | ||:|
Db         54 YQILNQDNFGLAAELGYDNFGRVKFRA---EGKTKAKHTNHGAHLSLKGSYEVLDGLDVY 110

Qy        109 TRLGGMVWRADSKGNYASTGV---SRSEHDTGVSPVFAGGVEWAVTRDIATRLEYQWVNN 165
               : |  : |:| |   |        :  |    | :|| | |:||  ::| |||||  :
Db        111 GKAGVALVRSDYKFYEAPNSTRDXKKGTHTARASGLFAVGAEYAVLPELAVRLEYQQLTR 170

Qy        166 IG-----DAGTVGTRPDN--------GMLSLGVSYRFGQEDAAPVVAPAPAPAPEVATKH 212
              :|      |        |:         | :: |:|||||  ||||              |
Db        171 VGKYRPQDKNAPSINPNTAIHYNPXIGSINAGISYRFGQ-GAAPV------------KT 216

Qy        213 FTLKSDVLFNFNKATLKPEGQQALDQLYTQLSNMDPKDGSAVVLGYTDRIGSEAYNQQLS 272
              |:|  || | | || |||: |  || :| ::| :  |      | ||||||||:|:| :||
Db        217 FSLNLDVTFAFGKANLKPQAQATLDSIYGEMSQV--KSAKVAVAGYTDRIGSDAFNVKLS 274

Qy        273 EKRAQSVVDYLVAKGIPAGKISARGMGESNPVTGNTCDNVKARAALIDCLAPDRRVEIEV 332
              ::|| || :| |||| |  ||| | |::||||| | | |  | |||  ||||||||| |
Db        275 QERADSVANYFVAKGVAADAISATGYGKANPVTGATXDQVWGRWALIATLAPDRRVEIAV 334

Qy        333 KGYK 336
              | |
Db        335 NGTK 338
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RESULT 15
US-08-836-500A-6
; Sequence 6, Application US/08836500A
; Patent No. 6197929
; GENERAL INFORMATION:
; APPLICANT: Binz, Hans
; APPLICANT: Baussant, Thierry
; APPLICANT: Haeuw, Jean-Francois
; APPLICANT: Nguyen Ngoc, Thien
; TITLE OF INVENTION: Carrier Protein Having an Adjuvant
; TITLE OF INVENTION: Effect, Immunogenic Complex Containing It, Process for
; TITLE OF INVENTION: Their Preparation, Nucleotide Sequence and Vaccines
; Patent No. 6197929
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rockey, Milnamow & Katz, Ltd.
; STREET: 180 N. Stetson, 2 Prudential Plaza, Suite
; STREET: 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/836,500A
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Katz, Martin L.
; REGISTRATION NUMBER: 25,011
; REFERENCE/DOCKET NUMBER: PIE1514P0180US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400

```
;      TELEFAX:  312-616-5460
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  72 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-836-500A-6

  Query Match             20.8%;  Score 379;  DB 3;  Length 72;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-30;
  Matches   72;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        117 RADSKGNYASTGVSRSEHDTGVSPVFAGGVEWAVTRDIATRLEYQWVNNIGDAGTVGTRP 176
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 RADSKGNYASTGVSRSEHDTGVSPVFAGGVEWAVTRDIATRLEYQWVNNIGDAGTVGTRP 60

Qy        177 DNGMLSLGVSYR 188
              ||||||||||||
Db         61 DNGMLSLGVSYR 72


Search completed: January 19, 2005, 18:17:29
Job time : 26 secs
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